

GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 10:21:51 ; Search time 350.903 Seconds

(Without alignments)
5225.021 Million cell updates/sec

Title: US-09-963-803-11

Perfect score: 63

Sequence: 1 ggcggaagaaacttaattgc.....tgcgcgtcccaagcttat 63

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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GenBndl:.*
1: gb_ba:.*
2: gb_htg:.*
3: gb_in:.*
4: gb_cm:.*
5: gb_ov:.*
6: gb_pac:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_stg:.*
12: gb_sy:.*
13: gb_un:.*
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15: em_ba:.*
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41: em_htg_other:.*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	63	6 AX036745	AX036745 Sequence
2	63	100.0	317	6 AX036737	AX036737 Sequence
3	63	100.0	371	6 AX036739	AX036739 Sequence
4	61.4	97.5	301	6 AX036741	AX036741 Sequence
5	61.4	97.5	348	6 AX036738	AX036738 Sequence
6	61.4	97.5	398	6 AX036740	AX036740 Sequence
7	42	66.7	243	6 AX036735	AX036735 Sequence
8	42	66.7	7489	14 CYMWGC	AX036735 Sequence
9	41.2	65.4	392	6 AX036755	AX036755 Sequence
10	38.8	61.6	604	6 AX036757	AX036757 Sequence
11	37	58.7	472	6 AX036759	AX036759 Sequence
12	37	58.7	541	6 AX036758	AX036758 Sequence
13	35.4	56.2	393	6 AX036753	AX036753 Sequence
14	35.4	56.2	462	6 AX036754	AX036754 Sequence
15	35.4	56.2	600	6 AX036756	AX036756 Sequence
16	35.4	56.2	9285	6 AX036756	AX036756 Sequence
17	35.4	56.2	15077	6 AX036756	AX036756 Sequence
18	35.4	56.2	15077	6 AX036756	AX036756 Sequence
19	27.4	43.5	65142	2 AC121501	AX036756 Sequence
20	27.4	43.5	109395	2 AC013742	AX036756 Sequence
21	27.4	43.5	128821	9 AC108687	AX036756 Sequence
22	27.4	43.5	134236	10 AC024883	AX036756 Sequence
23	27.4	43.5	158987	9 AC108713	AX036756 Sequence
24	26.8	42.5	174327	2 AC068159	AX036756 Sequence
25	26.8	42.5	155013	2 AC008954	AX036756 Sequence
26	26.8	42.5	129564	2 AC026707	AX036756 Sequence
27	26.6	42.2	167932	2 AC068133	AX036756 Sequence
28	26.6	42.2	167932	2 AC068133	AX036756 Sequence
29	26.2	41.6	241928	2 AC015846	AX036756 Sequence
30	26	41.3	10427	1 AE012158	AX036756 Sequence
31	25.6	40.6	168111	2 AC096061	AX036756 Sequence
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33	25.4	40.3	131796	9 AC097632	AX036756 Sequence
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35	25.2	40.0	189615	2 AC129390	AX036756 Sequence
36	24.8	39.4	539	6 AX062521	AX036756 Sequence
37	24.8	39.4	539	6 AX367438	AX036756 Sequence
38	24.8	39.4	1321	6 A02597	AX036756 Sequence
39	24.8	39.4	4530	1 BAC80XWF	AX036756 Sequence
40	24.8	39.4	89211	9 AL669821	AX036756 Sequence
41	24.8	39.4	129839	9 AL355591	AX036756 Sequence
42	24.8	39.4	161267	9 AC008378	AX036756 Sequence
43	24.8	39.4	201831	2 AC131112	AX036756 Sequence
44	24.6	39.0	95865	8 AC003970	AX036756 Sequence
45	24.6	39.0	146222	2 AC128643	AX036756 Sequence

ALIGNMENTS

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RESULT 1
AX036745 LOCUS AX036745 63 bp DNA
DEFINITION Sequence 11 from Patent WO0058485.
ACCESSION AX036745
VERSION AX036745.1 GI:11226254
KEYWORDS
SOURCE
ORGANISM
SYNTHETIC CONSTRUCT
ARTIFICIAL SEQUENCES
REFERENCE
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A II 05-OCT-2000;
```

MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES
source
1. .63
/db_xref="taxon:32630"
/note="Directional desoxy nucleotide building block S4"
BASE COUNT 14 a 14 c 15 g 20 t
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Best Local Similarity 100.0%; Pred. No. 9.7e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGAAAGTACCTTATGCTTGTAACTTGTACCCGCGTATGCCGTTCCCAAGCTT 60
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Db 1 GGGGAAAGTACCTTATGCTTGTAACTTGTACCCGCGTATGCCGTTCCCAAGCTT 60
QY 61 TAT 63
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Db 61 TAT 63
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RESULT 2
AX036737 317 bp DNA linear PAT 16-NOV-2000
LOCUS AX036737
DEFINITION Sequence 3 from Patent WO0058485.
ACCESSION AX036737
VERSION AX036737.1 GI:11226246
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 317)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 3 05-OCT-2000.
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES
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Location/Qualifiers
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/db_xref="taxon:32630"
/note="promoter Mp1116"
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Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGAAAGTACCTTATGCTTGTAACTTGTACCCGCGTATGCCGTTCCCAAGCTT 60
|||||
Db 195 GGGGAAAGTACCTTATGCTTGTAACTTGTACCCGCGTATGCCGTTCCCAAGCTT 254
QY 61 TAT 63
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Db 255 TAT 257
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RESULT 3
AX036739 371 bp DNA linear PAT 16-NOV-2000
LOCUS AX036739
DEFINITION Sequence 5 from Patent WO0058485.
ACCESSION AX036739
VERSION AX036739.1 GI:11226248
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 371)

AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 5 05-OCT-2000.
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES
source
1. .371
Location/Qualifiers
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/db_xref="taxon:32630"
/note="promoter Mp1116"
BASE COUNT 122 a 68 c 89 g 92 t
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Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGAAAGTACCTTATGCTTGTAACTTGTACCCGCGTATGCCGTTCCCAAGCTT 60
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QY 61 TAT 63
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Db 309 TAT 311
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RESULT 4
AX036741 301 bp DNA linear PAT 16-NOV-2000
LOCUS AX036741
DEFINITION Sequence 7 from Patent WO0058485.
ACCESSION AX036741
VERSION AX036741.1 GI:11226250
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 301)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 7 05-OCT-2000.
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES
source
1. .301
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter Mp11154"
BASE COUNT 98 a 54 c 74 g 75 t
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Query Match 97.5%; Score 61.4; DB 6; Length 301;
Best Local Similarity 98.4%; Pred. No. 5.4e-14;
Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGGAAAGTACCTTATGCTTGTAACTTGTACCCGCGTATGCCGTTCCCAAGCTT 60
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Db 181 GGGGAAAGTACCTTATGCTTGTAACTTGTACCCGCGTATGCCGTTCCCAAGCTT 240
QY 61 TAT 63
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Db 241 TAT 243
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RESULT 5
AX036738 348 bp DNA linear PAT 16-NOV-2000
LOCUS AX036738
DEFINITION Sequence 4 from Patent WO0058485.
ACCESSION AX036738
VERSION AX036738.1 GI:11226247

KEYWORDS	SYNTHETIC CONSTRUCT.
SOURCE	synthetic construct.
ORGANISM	synthetic construct
REFERENCE	artificial sequences.
AUTHORS	1 (bases 1 to 348)
TITLE	Rance, I., Theisen, M. and Gruber, V.
JOURNAL	Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus
Patent:	WO 0058485-A 4 05-OCT-2000;
MEISTEM THERAPEUTICS (FR)	
RANCE IANN (FR)	
THEISEN MANFRED (FR)	
GRUBER VERONIQUE (FR)	
Location/Qualifiers	
1..348	
/organism="synthetic construct"	
/db_xref="taxon:32630"	
/note="promoter Mp1147"	
1..398	
promoter	
128 a	80 c
93 g	97 t
BASE COUNT	
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Best Local Similarity	98.4%: Pred. No. 5.5e-14;
Matches 62; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1 GCGGGAAGTACCTTATGATTTGTACTTGGTTACCGGATGCGGTTCCCAAGCTT 60
Db	228 GCGGGAAGTACCTTATGATTTGTACTTGGTTACCGGATGCGGTTCCCAAGCTT 287
QY	61 TAT 63
Db	288 TAT 290
RESULT 6	
LOCUS	AX036740 398 bp DNA linear PAT 16-NOV-2000
DEFINITION	Sequence 6 from Patent WO0058485.
ACCESSION	AX036740
VERSION	AX036740.1 GI:11226249
KEYWORDS	
SOURCE	synthetic construct.
ORGANISM	artificial construct
REFERENCE	artificial sequences.
AUTHORS	1 (bases 1 to 398)
TITLE	Rance, I., Theisen, M. and Gruber, V.
JOURNAL	Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus
Patent:	WO 0058485-A 6 05-OCT-2000;
MEISTEM THERAPEUTICS (FR)	
RANCE IANN (FR)	
THEISEN MANFRED (FR)	
GRUBER VERONIQUE (FR)	
Location/Qualifiers	
1..398	
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/note="promoter Mp1147"	
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128 a	80 c
93 g	97 t
BASE COUNT	
ORIGIN	
Query Match	97.5%: Score 61.4; DB 6; Length 398;
Best Local Similarity	98.4%: Pred. No. 5.6e-14;
Matches 62; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1 GCGGGAAGTACCTTATGATTTGTACTTGGTTACCGGATGCGGTTCCCAAGCTT 60
Db	278 GCGGGAAGTACCTTATGATTTGTACTTGGTTACCGGATGCGGTTCCCAAGCTT 337
QY	61 TAT 63
Db	338 TAT 340

LOCUS	AX036735	243 bp	DNA	linear	PAT 16-NOV-2000
DEFINITION	Sequence 1 from Patent WO0058485.				
ACCESSION	AX036735				
VERSION	AX036735.1				
KEYWORDS	GI:11226244				
SOURCE					
ORGANISM	synthetic construct.				
REFERENCE	artificial sequences.				
AUTHORS	1 (bases 1 to 243)				
TITLE	Rance, I., Theisen, M. and Gruber, V.				
JOURNAL	Chemice expression promoters originating from commelina yellow				
	mottle virus and cassava vein mosaic virus				
	Patent: WO 0058485-A 1 05-0CT-2000;				
	MEISTERM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)				
	; GRUBER VERONIQUE (FR)				
FEATURES	Location/Qualifiers				
source	1..243				
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	of Commelina yellow Mottle Virus"				
promoter	1..243				
BASE COUNT	71 a 53 c 45 g 74 t				
ORIGIN					
Query Match	66.7%; Score 42; DB 6; Length 243;				
Best Local Similarity	100.0%; Pred. No. 4.2e-06;				
Matches	42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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Db	153 TTTGTACTTGTTACCGGATAGCCGGTCCCAAGCTTTAT 194				
RESULT 8					
CYMWCG					
LOCUS	CYMWCG	7489 bp	DNA	linear	VRL 12-SEP-1993
DEFINITION	Commelina yellow mottle virus complete circular genome.				
ACCESSION	X52938				
VERSION	X52938.1				
KEYWORDS	GI:59047				
SOURCE	complete genome; protease; reverse transcriptase; ribonuclease H.				
ORGANISM	Commelina yellow mottle virus.				
REFERENCE	Commelina yellow mottle virus.				
AUTHORS	1 (bases 1 to 7489)				
TITLE	Viruses; Retroid viruses; Caulimoviridae; Badnavirus.				
JOURNAL	1 (bases 1 to 7489)				
	Oliszewski, N.E.				
	Direct Submission				
	Submitted (02-MAY-1990) Oliszewski N.E., University of Minnesota,				
	Dept of Plant Biology, 220 Biological Sciences Center, 1445 Gortner				
	Ave., St. Paul, MN 55108, USA				
REMARK	(revised by [41])				
REFERENCE	2 (bases 1 to 7489)				
AUTHORS	Medberry, S.L., Lockhart, B.E. and Oliszewski, N.E.				
TITLE	Properties of Commelina yellow mottle virus's complete DNA				
	sequence, genomic discontinuities and transcript suggest that it is				
	a pararetrovirus				
	Nucleic Acids Res. 18 (18), 5505-5513 (1990)				
JOURNAL					
MEDLINE	91016835				
PUBMED	1699203				
REFERENCE	3 (bases 1 to 7489)				
AUTHORS	Oliszewski, N.E.				
TITLE	Direct Submission				
JOURNAL	Submitted (29-NOV-1990) Oliszewski N.E., University of Minnesota,				
	Dept of Plant Biology, 220 Biological Sciences Center, 1445 Gortner				
	Ave., St. Paul, MN 55108, USA				
REFERENCE	4 (bases 1 to 7489)				
AUTHORS	Oliszewski, N.E.				
TITLE	Direct Submission				
JOURNAL	Submitted (07-DEC-1990)				
COMMENT	[3] The extra c at position 2672 permits readthrough to result in				
	one				
	ORF (216 kD protein) rather than two (47 kD ORF and 163 kD ORF).				

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FEATURES
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                /organism="Commelina yellow mottle virus"
                /db_xref="taxon:10653"
                /clone="pcoymv89 (and pcoymv89)"
            1..23
                /product="trna-met"
                /note="put. trna-met (put. primer for minus strand synthesis)"
            300..302
                /note="gac was cga"
                /citation=[1]
            496..1098
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                RISEQPKFKEQTELTLELKLVEEVAKLIHSFKGMVN"
            541
                /note="t in clone pcoymv100"
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                GGRLLSTMPGVSSSERTLEMQMNPVQLOSGMNRARAVREVIIRTPKSVNHRV
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                KOAOEPTIOEELPTHEQNPBEIQNEIHFEEPAFKHLAQLSELVMASSGSG
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                NSKITSKFDKSGFMVAAEESVPTALAKNKLIEWLVMPGLKNAATPORKNDN
                VKGTGEKFLAIVLIDILVFSEAEQSHQSLTYMLQDCKNGILSTPKKKIKITPELD
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Query Match      66.7%: Score 42; DB 14; Length 7489;
Best Local Similarity 100.0%: Pred. No. 6.6e-06;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 22 TTGTACTGTGTTACCGGTATCGCGTCCCAAGTTTAT 63
Db 7276 TTGTACTGTGTTACCGGTATCGCGTCCCAAGTTTAT 7317

RESULT 9
AX036755 392 bp DNA 1linear PAT 16-NOV-2000
LOCUS AX036755 Sequence 21 from Patent WO0058485.
DEFINITION AX036755
ACCESSION AX036755
VERSION AX036755.1 GI:11226264
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 392)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow
JOURNAL mottle virus and cassava vein mosaic virus
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
FEATURES
    source
        Location/Qualifiers
            1..392
                /organism="synthetic construct"
                /db_xref="taxon:32630"
                /note="promoter MP-1164"
            127 a 80 c 87 g 98 t
            promoter 127 a 80 c 87 g 98 t
            BASE COUNT 127 a 80 c 87 g 98 t
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                Query Match      65.4%: Score 41.2; DB 6; Length 392;
                Best Local Similarity 79.0%: Pred. No. 9.4e-06;
                Matches 49; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Oy 1 GGGGAAAGTAACCTTATGATTTGTAACCTTGTACCCGGTATGCCGGTTCCCAAGCTT 60
Db 197 GGGGAAAGTAACCTTATGATTTGTAACCTTGTACCGTATGCCGGTATCCCTTAAGT 256

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Oy 61 TA 62
Db 257 CA 258

RESULT 10
LOCUS AX036757 604 bp DNA Linear PAT 16-NOV-2000

DEFINITION Sequence 23 from Patent WO0058485.
ACCESSION AX036757
VERSION AX036757.1 GI:11226266

KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequences.

REFERENCE
1 (bases 1 to 604)
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 23 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)

FEATURES
source location/Qualifiers
1..604

promoter
BASE COUNT 186 a 116 c 145 g 157 t
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1..604
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter MPr1167"

Query Match
Best Local Similarity 95.2%; Score 38.8; DB 6; Length 604;
Matches 40; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GGCGAAAGTAACTTATGACTTGTACTGTTACCCGCT 42
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Db 278 GGCGAAAGTAACTTATGACTTGTACTGTTACTACT 319

RESULT 11
LOCUS AX036759 472 bp DNA Linear PAT 16-NOV-2000

DEFINITION Sequence 25 from Patent WO0058485.
ACCESSION AX036759
VERSION AX036759.1 GI:11226268

KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequences.

REFERENCE
1 (bases 1 to 472)
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 25 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)

FEATURES
source location/Qualifiers
1..472

promoter
BASE COUNT 149 a 92 c 112 g 119 t
ORIGIN
1..472
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter MPr1169"

Query Match
Best Local Similarity 100.0%; Score 37; DB 6; Length 472;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGCGAAAGTAACTTATGACTTGTACTGTTAC 37
|||||

Db 278 GGCGAAAGTAACTTATGACTTGTACTGTTAC 314

RESULT 12
LOCUS AX036758 541 bp DNA Linear PAT 16-NOV-2000

DEFINITION Sequence 24 from Patent WO0058485.
ACCESSION AX036758
VERSION AX036758.1 GI:11226267

KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequences.

REFERENCE
1 (bases 1 to 541)
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 24 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)

FEATURES
source location/Qualifiers
1..541

promoter
BASE COUNT 169 a 104 c 130 g 138 t
ORIGIN
1..541
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter MPr1168"

Query Match
Best Local Similarity 100.0%; Score 37; DB 6; Length 541;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGCGAAAGTAACTTATGACTTGTACTGTTAC 37
|||||
Db 278 GGCGAAAGTAACTTATGACTTGTACTGTTAC 314

RESULT 13
LOCUS AX036753 393 bp DNA Linear PAT 16-NOV-2000

DEFINITION Sequence 19 from Patent WO0058485.
ACCESSION AX036753
VERSION AX036753.1 GI:11226262

KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequences.

REFERENCE
1 (bases 1 to 393)
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 19 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)

FEATURES
source location/Qualifiers
1..393

promoter
BASE COUNT 128 a 75 c 93 g 97 t
ORIGIN
1..393
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter MPr1162"

Query Match
Best Local Similarity 97.3%; Score 35.4; DB 6; Length 393;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GGCGAAAGTAACTTATGACTTGTACTGTTAC 37
|||||
Db 197 GGCGAAAGTAACTTATGACTTGTACTGTTAC 233

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 07:18:51 ; Search time 108.726 Seconds
(without alignments)
1304.896 Million cell updates/sec

Title: US-09-963-803-11

Perfect score: 63

Sequence: 1 ggcggaagaacttatgc.....tgcgcgttcccaagcttat 63

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	63	21	AAA96845
2	63	100.0	317	21	AAA96837
3	63	100.0	317	21	AAA96839
4	61.4	97.5	301	21	AAA96841
5	61.4	97.5	348	21	AAA96838
6	61.4	97.5	398	21	AAA96840
7	42	66.7	243	21	AAA96835
8	41.2	65.4	392	21	AAA96855
9	38.8	61.6	604	21	AAA96857

10	37	58.7	472	21	AAA96859	Nucleotide sequenc
11	37	58.7	541	21	AAA96858	Nucleotide sequenc
12	35.4	56.2	393	21	AAA96853	Nucleotide sequenc
13	35.4	56.2	462	21	AAA96854	Nucleotide sequenc
14	35.4	56.2	600	21	AAA96856	Nucleotide sequenc
15	24.8	39.4	434	24	ABL79935	Human ovarian canc
16	24.8	39.4	539	22	AAAF68230	Human lung tumour
17	24.8	39.4	539	24	ABK38141	CDNA encoding clon
18	24.8	39.4	777	23	AA567507	DNA encoding novel
19	24.8	39.4	2551	9	AAAB1551	Bio F, Bio C and B
20	24.6	39.0	1449	9	AAAC43051	Arabidopsis thalia
21	24.6	39.0	1506	21	AAAC49145	Arabidopsis thalia
22	24	38.1	2765	23	ABLI4808	Arabidopsis thalia
23	23.4	37.1	2413	24	ABNB8295	Human large protei
24	23.2	36.8	1461	22	AAH29763	S cerevisiae apopt
25	23.2	36.8	3411	23	ABL28884	Drosophila melanog
26	22.8	36.2	748	21	AAAC44959	Arabidopsis thalia
27	22.8	36.2	888	21	AAAC35439	Arabidopsis thalia
28	22.6	35.9	6565	23	ABLI8414	Drosophila melanog
29	22.4	35.6	347	24	ABLB8625	Human ovarian canc
30	22.4	35.6	12010	24	ABNB6827	Gene #3370 used to
31	22.4	35.6	13857	22	AAK82827	Human immune/hema
32	22.2	35.2	220	21	AAK45410	Human secreted exp
33	22.2	35.2	375	22	AAH52940	S. epidermidis ope
34	22.2	35.2	562	22	ABA09445	Human IGERB homolo
35	22.2	35.2	627	22	AAH52365	S. epidermidis ope
36	22.2	35.2	771	24	ABK75564	Bacillus lichenifo
37	22.2	35.2	841	22	AAAL5716	Human breast cance
38	22.2	35.2	1312	22	AAFS9199	Human MyoD1 gene p
39	22.2	35.2	1330	21	AAAI6693	Human secreted pro
40	22.2	35.2	1563	21	AAZ36238	cDNA encoding a bo
41	22.2	35.2	1669	20	AAK15104	High affinity immu
42	22.2	35.2	1670	21	AAZ32842	Human high affinity
43	22.2	35.2	1769	21	ABL90726	Human polynucleoti
44	22.2	35.2	2021	22	AAFS9183	Human MyoD1 gene p
45	22.2	35.2	2284	22	AAFS9182	Human MyoD1 gene p

ALIGNMENTS

RESULT 1	AAA96845	standard; DNA; 63 BP.
ID	AAA96845	
AC	AAA96845;	
XX		
DT	19-FEB-2001	(first entry)
XX		
DE	Directional desoxynucleotide building block S4.	
XX		
KW	Promoter; Intergenic region; Commelina yellow mottle virus;	
KW	Chimeric expression promoter; plant vascular expression promoter;	
KW	plant green tissue expression promoter; Cassava vein mosaic virus;	
KW	transgenic plant; ss.	
OS	Synthetic.	
PN	WO200058485-A1.	
XX		
PD	05-OCT-2000.	
XX		
PF	29-MAR-2000; 2000WO-IB00370.	
XX		
PR	29-MAR-1999; 99FR-0003925.	
XX		
PA	(MERI-) MERISTEM THERAPEUTICS.	
XX		
PI	Rance I, Gruber V, Theisen M;	
XX		
DR	WPI: 2000-647238/62.	
XX		
PT	Chimeric expression promoter for transgenic plant production, comprises	

PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX Disclosure; Page 23; 91pp; English.
XX
CC The present sequence represents a directional desoxyribonucleotide building
CC block, which was used to construct chimeric promoters of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC commelina yellow mottle virus, and the second plant promoter originates
CC from the cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 63 BP; 14 A; 14 C; 15 G; 20 T; 0 other;
Query Match 100.0%; Score 63; DB 21; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.8e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGGAAGTACCTTGTGATTTGTACTTGGTTACCGCGTATGCCGGTTCCCAAGCTT 60
DB 1 GGGGGAAGTACCTTGTGATTTGTACTTGGTTACCGCGTATGCCGGTTCCCAAGCTT 60
QY 61 TAT 63
DB 61 TAT 63
DB 61 TAT 63
RESULT 2
ID AAA96837 standard; DNA: 317 BP.
XX
AC AAA96837;
XX
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter MP1116.
XX
KW Promoter: intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KW transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
PN WO200058485-A1.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000MO-IB00370.
XX
PR 29-MAR-1999; 99PR-0003925.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI; 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX Claim 5; Page 81; 91pp; English.

CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC commelina yellow mottle virus, and the second plant promoter originates
CC from the cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 317 BP; 107 A; 61 C; 74 G; 75 T; 0 other;
Query Match 100.0%; Score 63; DB 21; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGGAAGTACCTTGTGATTTGTACTTGGTTACCGCGTATGCCGGTTCCCAAGCTT 60
DB 195 GGGGGAAGTACCTTGTGATTTGTACTTGGTTACCGCGTATGCCGGTTCCCAAGCTT 254
QY 61 TAT 63
DB 255 TAT 257
RESULT 3
ID AAA96839 standard; DNA: 371 BP.
XX
AC AAA96839;
XX
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter MP1146.
XX
KW Promoter: intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KW transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
PN WO200058485-A1.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000MO-IB00370.
XX
PR 29-MAR-1999; 99PR-0003925.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI; 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX Claim 5; Page 81; 91pp; English.
XX
CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC promoter region. Especially, the promoters are useful
CC for producing transgenic plants.

CC Commelina yellow mottle virus, and the second plant promoter originates
 CC from the Cassava vein mosaic virus. Especially, the promoters are
 CC derived from intergenic regions. The chimeric promoters are useful
 CC for producing transgenic plants.

SO Sequence 371 BP; 122 A; 68 C; 89 G; 92 T; 0 other;

Query Match 100.0%; Score 63; DB 21; Length 371;

Best Local Similarity 100.0%; Pred. No. 4e-15; Mismatches 0; Indels 0; Gaps 0;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 GCGGGAAGTAACCTTATGCACTTGTACCTGTTACCCGGTATCCGCTTCCCAAGCTT 60

DB 249 GCGGGAAGTAACCTTATGCACTTGTACCTGTTACCCGGTATCCGCTTCCCAAGCTT 308

OY 61 TAT 63

DB 309 TAT 311

RESULT 4
 AAA96841
 ID AAA96841 standard; DNA; 301 BP.

AC AAA96841;

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MPr1154.

OS Promoter; intergenic region; Commelina yellow mottle virus;

KW chimeric expression promoter; plant vascular expression promoter;

KM plant green tissue expression promoter; Cassava vein mosaic virus;

OS Chimeric - Commelina yellow mottle virus.

OS Chimeric - Cassava vein mosaic virus.

PN WO200058485-A1.

PD 05-OCT-2000.

PF 29-MAR-2000; 2000WO-IB00370.

PR 29-MAR-1999; 99FR-0003925.

PA (MERT-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Theisen M;

PT WPI; 2000-647238/62.

PT Chimeric expression promoter for transgenic plant production, comprises

PT sequence from promoter comprising vascular expression region replaced

PT with sequence from promoter comprising green tissue expression region

PS Claim 5; Page 82; 91pp; English.

CC The present sequence represents a chimeric promoter of the invention.

CC The specification describes chimeric expression promoters. These

CC chimeric promoters comprise a nucleic acid sequence which is derived

CC from a first plant promoter, in which a plant vascular expression

CC promoter region is replaced with a nucleic acid sequence derived from

CC a second plant promoter comprising a plant green tissue expression

CC promoter region. Preferably, the first plant promoter originates from

CC Commelina yellow mottle virus, and the second plant promoter originates

CC from the Cassava vein mosaic virus. Especially, the promoters are

CC derived from intergenic regions. The chimeric promoters are useful

CC for producing transgenic plants.

Query Match 97.5%; Score 61.4; DB 21; Length 301;

Best Local Similarity 98.4%; Pred. No. 1.6e-14; Mismatches 1; Indels 0; Gaps 0;

Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 GCGGGAAGTAACCTTATGCACTTGTACCTGTTACCCGGTATCCGCTTCCCAAGCTT 240

OY 61 TAT 63

DB 241 TAT 243

RESULT 5
 AAA96838
 ID AAA96838 standard; DNA; 348 BP.

AC AAA96838;

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MPr1117.

OS Promoter; intergenic region; Commelina yellow mottle virus;

KW chimeric expression promoter; plant vascular expression promoter;

KM plant green tissue expression promoter; Cassava vein mosaic virus;

OS Chimeric - Commelina yellow mottle virus.

OS Chimeric - Cassava vein mosaic virus.

PN WO200058485-A1.

PD 05-OCT-2000.

PF 29-MAR-2000; 2000WO-IB00370.

PR 29-MAR-1999; 99FR-0003925.

PA (MERT-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Theisen M;

PT WPI; 2000-647238/62.

PT Chimeric expression promoter for transgenic plant production, comprises

PT sequence from promoter comprising vascular expression region replaced

PT with sequence from promoter comprising green tissue expression region

PS Claim 5; Page 81; 91pp; English.

CC The present sequence represents a chimeric promoter of the invention.

CC The specification describes chimeric expression promoters. These

CC chimeric promoters comprise a nucleic acid sequence which is derived

CC from a first plant promoter, in which a plant vascular expression

CC promoter region is replaced with a nucleic acid sequence derived from

CC a second plant promoter comprising a plant green tissue expression

CC promoter region. Preferably, the first plant promoter originates from

CC Commelina yellow mottle virus, and the second plant promoter originates

CC from the Cassava vein mosaic virus. Especially, the promoters are

CC derived from intergenic regions. The chimeric promoters are useful

CC for producing transgenic plants.

SO Sequence 348 BP; 116 A; 70 C; 78 G; 84 T; 0 other;

Query Match 97.5%; Score 61.4; DB 21; Length 348;

Best Local Similarity 98.4%; Pred. No. 1.7e-14; Mismatches 1; Indels 0; Gaps 0;

Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 GCGGGAAGTAACCTTATGCACTTGTACCTGTTACCCGGTATCCGCTTCCCAAGCTT 60

DB 228 GCGGGAAGTAACCTTATGCACTTGTACCTGTTACCCGGTATCCGCTTCCCAAGCTT 287

OY 61 TAT 63
 DB 288 TAT 290

RESULT 6
 AAA96840
 ID AAA96840 standard; DNA; 398 BP.

AC AAA96840;
 XX
 DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MP1147.

XX Promoter; intergenic region; Commelina yellow mottle virus;
 KM chimeric expression promoter; plant vascular expression promoter;
 KM plant green tissue expression promoter; cassava vein mosaic virus;
 KM transgenic plant; chimera; ss.

XX Chimeric - Commelina yellow mottle virus.
 OS Chimeric - Cassava vein mosaic virus.

XX MO200058485-A1.

PD 05-OCT-2000.

PF 29-MAR-2000; 2000WO-IB00370.

PR 29-MAR-1999; 99FR-0003925.

PA (MERI-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Theisen M;

XX WPI; 2000-647238/62.

PT Chimeric expression promoter for transgenic plant production, comprises
 PT sequence from promoter comprising vascular expression region replaced
 PT with sequence from promoter comprising green tissue expression region

XX Claim 5; Page 82; 91pp; English.

CC The present sequence represents a chimeric promoter of the invention.
 CC The specification describes chimeric expression promoters. These
 CC chimeric promoters comprise a nucleic acid sequence which is derived
 CC from a first plant promoter, in which a plant vascular expression
 CC promoter region is replaced with a nucleic acid sequence derived from
 CC a second plant promoter comprising a plant green tissue expression
 CC promoter region. Preferably, the first plant promoter originates from
 CC Commelina yellow mottle virus, and the second plant promoter originates
 CC from the Cassava vein mosaic virus. Especially, the promoters are
 CC derived from intergenic regions. The chimeric promoters are useful
 CC for producing transgenic plants.

XX Sequence 398 BP; 128 A; 80 C; 93 G; 97 T; 0 other;

Query Match 97.5%; Score 61.4; DB 21; Length 398;
 Best Local Similarity 98.4%; Pred. No. 1.7e-14;
 Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGGAAAGTAACTTATGCTTGAACCTGTTACCGGATGCGGTTCCCAAGCTT 60
 DB 278 GGGGAAAGTAACTTATGCTTGAACCTGTTACCGGATGCGGTTCCCAAGCTT 337

OY 61 TAT 63
 DB 338 TAT 340

RESULT 7

AAA96835
 ID AAA96835 standard; DNA; 243 BP.

AC AAA96835;

DT 19-FEB-2001 (first entry)

DE Promoter from intergenic region of Commelina yellow mottle virus.

XX Promoter; intergenic region; Commelina yellow mottle virus;
 KM chimeric expression promoter; plant vascular expression promoter;
 KM plant green tissue expression promoter; cassava vein mosaic virus;
 KM transgenic plant; ss.

OS Commelina yellow mottle virus.

PN MO200058485-A1.

PD 05-OCT-2000.

PF 29-MAR-2000; 2000WO-IB00370.

PR 29-MAR-1999; 99FR-0003925.

PA (MERI-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Theisen M;

XX WPI; 2000-647238/62.

PT Chimeric expression promoter for transgenic plant production, comprises
 PT sequence from promoter comprising vascular expression region replaced
 PT with sequence from promoter comprising green tissue expression region

XX Claim 4; Page 79; 91pp; English.

CC The present sequence represents a promoter fragment from the intergenic
 CC region of Commelina yellow mottle virus. The promoter is a strong
 CC promoter in vascular and reproductive tissues. The promoter is used to
 CC construct chimeric expression promoters. These chimeric promoters
 CC comprise a nucleic acid sequence which is derived from a first
 CC plant promoter, in which a plant vascular expression promoter region is
 CC replaced with a nucleic acid sequence derived from a second plant
 CC promoter comprising a plant green tissue expression promoter region.
 CC Preferably, the first plant promoter originates from Commelina yellow
 CC mottle virus, and the second plant promoter originates from the Cassava
 CC vein mosaic virus. The chimeric promoters are useful for producing
 CC transgenic plants.

XX Sequence 243 BP; 71 A; 53 C; 45 G; 74 T; 0 other;

Query Match 66.7%; Score 42; DB 21; Length 243;
 Best Local Similarity 100.0%; Pred. No. 7.2e-07;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 TTTGTAACTGTTACCGGATGCGGTTCCCAAGCTTAT 63
 DB 153 TTTGTAACTGTTACCGGATGCGGTTCCCAAGCTTAT 194

RESULT 8
 AAA96855
 ID AAA96855 standard; DNA; 392 BP.

AC AAA96855;

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MP1164.

XX Promoter; intergenic region; Commelina yellow mottle virus;
 KM chimeric expression promoter; plant vascular expression promoter;

KW plant green tissue expression promoter; Cassava vein mosaic virus;
 XX transgenic plant; chimera; ss.
 OS Chimeric - Commelina yellow mottle virus.
 OS Chimeric - Cassava vein mosaic virus.
 XX
 PN WO200058485-A1.
 XX
 PD 05-OCT-2000.
 XX
 PF 29-MAR-2000; 2000WO-IB00370.
 XX
 PR 29-MAR-1999; 99FR-0003925.
 XX
 PA (MERI-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theisen M;
 XX
 DR WPI: 2000-647238/62.
 XX
 PT Chimeric expression promoter for transgenic plant production, comprises
 PT sequence from promoter comprising vascular expression region replaced
 PT with sequence from promoter comprising green tissue expression region
 XX
 PS Claim 5; Page 86; 91pp; English.
 XX
 CC The present sequence represents a chimeric promoter of the invention.
 CC The specification describes chimeric expression promoters. These
 CC chimeric promoters comprise a nucleic acid sequence which is derived
 CC from a first plant promoter, in which a plant vascular expression
 CC promoter region is replaced with a nucleic acid sequence derived from
 CC a second plant promoter comprising a plant green tissue expression
 CC promoter region. Preferably, the first plant promoter originates from
 CC Commelina yellow mottle virus, and the second plant promoter originates
 CC from the Cassava vein mosaic virus. Especially, the promoters are
 CC derived from intergenic regions. The chimeric promoters are useful
 CC for producing transgenic plants.
 XX
 SQ Sequence 392 BP; 127 A; 80 C; 87 G; 98 T; 0 other;
 XX
 Query Match 65.4%; Score 41.2; DB 21; Length 392;
 Best Local Similarity 79.0%; Pred. No. 1.6e-06;
 Matches 49; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 XX
 OY 1 GCGGAAAGTACCTTATGCACTTGTACTGTACCGGATGCCGGTCCCAAGCT 60
 DB 197 GCGGAAAGTACCTTATGCACTTGTACTGTACCGGATGCCGGTCCCAAGCT 256
 XX
 OY 61 TA 62
 DB 257 CA 258
 XX
 RESULT 9
 AAA96857
 ID AAA96857 standard; DNA; 604 BP.
 XX
 AC AAA96857;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 DE Nucleotide sequence of chimeric expression promoter MP1167.
 XX
 KW Promoter; intergenic region; Commelina yellow mottle virus;
 KW chimeric expression promoter; plant vascular expression promoter;
 KW plant green tissue expression promoter; Cassava vein mosaic virus;
 KW transgenic plant; chimera; ss.
 XX
 OS Chimeric - Commelina yellow mottle virus.
 OS Chimeric - Cassava vein mosaic virus.
 XX
 PN WO200058485-A1.

XX
 PD 05-OCT-2000.
 XX
 PF 29-MAR-2000; 2000WO-IB00370.
 XX
 PR 29-MAR-1999; 99FR-0003925.
 XX
 PA (MERI-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theisen M;
 XX
 DR WPI: 2000-647238/62.
 XX
 PT Chimeric expression promoter for transgenic plant production, comprises
 PT sequence from promoter comprising vascular expression region replaced
 PT with sequence from promoter comprising green tissue expression region
 XX
 PS Claim 5; Page 87; 91pp; English.
 XX
 CC The present sequence represents a chimeric promoter of the invention.
 CC The specification describes chimeric expression promoters. These
 CC chimeric promoters comprise a nucleic acid sequence which is derived
 CC from a first plant promoter, in which a plant vascular expression
 CC promoter region is replaced with a nucleic acid sequence derived from
 CC a second plant promoter comprising a plant green tissue expression
 CC promoter region. Preferably, the first plant promoter originates from
 CC Commelina yellow mottle virus, and the second plant promoter originates
 CC from the Cassava vein mosaic virus. Especially, the promoters are
 CC derived from intergenic regions. The chimeric promoters are useful
 CC for producing transgenic plants.
 XX
 SQ Sequence 604 BP; 186 A; 116 C; 145 G; 157 T; 0 other;
 XX
 Query Match 61.6%; Score 38.8; DB 21; Length 604;
 Best Local Similarity 95.2%; Pred. No. 1.6e-05;
 Matches 40; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 OY 1 GCGGAAAGTACCTTATGCACTTGTACTGTACCGGAT 42
 DB 278 GCGGAAAGTACCTTATGCACTTGTACTGTACCGGAT 319
 XX
 RESULT 10
 AAA96859
 ID AAA96859 standard; DNA; 472 BP.
 XX
 AC AAA96859;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 DE Nucleotide sequence of chimeric expression promoter MP1169.
 XX
 KW Promoter; intergenic region; Commelina yellow mottle virus;
 KW chimeric expression promoter; plant vascular expression promoter;
 KW plant green tissue expression promoter; Cassava vein mosaic virus;
 KW transgenic plant; chimera; ss.
 XX
 OS Chimeric - Commelina yellow mottle virus.
 OS Chimeric - Cassava vein mosaic virus.
 XX
 PN WO200058485-A1.
 XX
 PD 05-OCT-2000.
 XX
 PF 29-MAR-2000; 2000WO-IB00370.
 XX
 PR 29-MAR-1999; 99FR-0003925.
 XX
 PA (MERI-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theisen M;
 XX

DR WPI; 2000-647238/62.
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX Claim 5; Page 88; 91pp; English.
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Comelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 472 BP; 149 A; 92 C; 112 G; 119 T; 0 other;
XX
Query Match 58.7%; Score 37; DB 21; Length 472;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGGGAAGTACCTTATGCACTTGTAACTGGTTAC 37
DB 278 GCGGGAAGTACCTTATGCACTTGTAACTGGTTAC 314
RESULT 11
AAA96858
ID AAA96858 standard; DNA; 541 BP.
XX
AC AAA96858;
XX
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter MP-1168.
XX
XX Promoter: intergenic region; Comelina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX
XX Chimeric - Comelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
OS
XX
PN WO200058485-A1.
XX
PD .05-OCT-2000.
XX
PF 29-MAR-2000; 2000MO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
XX (MER-) MERISTEM THERAPEUTICS.
XX
XX Rance I, Gruber V, Theisen M;
XX
XX WPI; 2000-647238/62.
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX Claim 5; Page 87-88; 91pp; English.
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These

CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Comelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 541 BP; 169 A; 104 C; 130 G; 138 T; 0 other;
XX
Query Match 58.7%; Score 37; DB 21; Length 541;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGGGAAGTACCTTATGCACTTGTAACTGGTTAC 37
DB 278 GCGGGAAGTACCTTATGCACTTGTAACTGGTTAC 314
RESULT 12
AAA96853
ID AAA96853 standard; DNA; 393 BP.
XX
AC AAA96853;
XX
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter MP-1162.
XX
XX Promoter: intergenic region; Comelina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX
XX Chimeric - Comelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
OS
XX
PN WO200058485-A1.
XX
PD .05-OCT-2000.
XX
PF 29-MAR-2000; 2000MO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
XX (MER-) MERISTEM THERAPEUTICS.
XX
XX Rance I, Gruber V, Theisen M;
XX
XX WPI; 2000-647238/62.
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX Claim 5; Page 85; 91pp; English.
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Comelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 393 BP; 128 A; 75 C; 93 G; 97 T; 0 other;

Query Match 56.2%; Score 35.4; DB 21; Length 393;
 Best Local Similarity 97.3%; Pred. No. 0.00032;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCGGAAAGTACCTTATGCACTTGTGTTAC 37
 |||||
 DB 197 GCGGAAAGTACCTTATGCACTTGTGTTAC 233

RESULT 13
 AAA96854
 ID AAA96854 standard; DNA; 462 BP.

XX AAA96854;

XX 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MP1163.

XX Promoter; intergenic region; Commelina yellow mottle virus;

KM chimeric expression promoter; plant vascular expression promoter;

KM plant green tissue expression promoter; cassava vein mosaic virus;

XX transgenic plant; chimera; ss.

OS Chimeric - Commelina yellow mottle virus.

XX Chimeric - Cassava vein mosaic virus.

XX WO200058485-A1.

XX 05-OCT-2000.

XX 29-MAR-2000; 2000WO-IB00370.

XX 29-MAR-1999; 99FR-0003925.

XX (MERI-) MERISTEM THERAPEUTICS.

XX Rance I, Gruber V, Theisen M;

XX WPI; 2000-647238/62.

XX Chimeric expression promoter for transgenic plant production, comprises

XX sequence from promoter comprising vascular expression region replaced

XX PT with sequence from promoter comprising green tissue expression region

XX PT

XX Claim 5; Page 86; 91pp; English.

XX The present sequence represents a chimeric promoter of the invention.

XX CC The specification describes chimeric expression promoters. These

XX CC chimeric promoters comprise a nucleic acid sequence which is derived

XX CC from a first plant promoter, in which a plant vascular expression

XX CC promoter region is replaced with a nucleic acid sequence derived from

XX CC a second plant promoter comprising a plant green tissue expression

XX CC promoter region. Preferably, the first plant promoter originates from

XX CC Commelina yellow mottle virus, and the second plant promoter originates

XX CC from the Cassava vein mosaic virus. Especially, the promoters are

XX CC derived from intergenic regions. The chimeric promoters are useful

XX CC for producing transgenic plants.

XX SQ Sequence 462 BP; 148 A; 87 C; 111 G; 116 T; 0 other;

XX Query Match 56.2%; Score 35.4; DB 21; Length 462;

XX Best Local Similarity 97.3%; Pred. No. 0.00033;

XX Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX OY 1 GCGGAAAGTACCTTATGCACTTGTGTTAC 37

XX |||||

XX DB 197 GCGGAAAGTACCTTATGCACTTGTGTTAC 233

XX RESULT 14

AAA96856
 ID AAA96856 standard; DNA; 600 BP.

XX AAA96856;

XX 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MP1165.

XX Promoter; intergenic region; Commelina yellow mottle virus;

KM chimeric expression promoter; plant vascular expression promoter;

KM plant green tissue expression promoter; cassava vein mosaic virus;

XX transgenic plant; chimera; ss.

OS Chimeric - Commelina yellow mottle virus.

XX Chimeric - Cassava vein mosaic virus.

XX WO200058485-A1.

XX 05-OCT-2000.

XX 29-MAR-2000; 2000WO-IB00370.

XX 29-MAR-1999; 99FR-0003925.

XX (MERI-) MERISTEM THERAPEUTICS.

XX Rance I, Gruber V, Theisen M;

XX WPI; 2000-647238/62.

XX Chimeric expression promoter for transgenic plant production, comprises

XX sequence from promoter comprising vascular expression region replaced

XX PT with sequence from promoter comprising green tissue expression region

XX PT

XX Claim 5; Page 86-87; 91pp; English.

XX The present sequence represents a chimeric promoter of the invention.

XX CC The specification describes chimeric expression promoters. These

XX CC chimeric promoters comprise a nucleic acid sequence which is derived

XX CC from a first plant promoter, in which a plant vascular expression

XX CC promoter region is replaced with a nucleic acid sequence derived from

XX CC a second plant promoter comprising a plant green tissue expression

XX CC promoter region. Preferably, the first plant promoter originates from

XX CC Commelina yellow mottle virus, and the second plant promoter originates

XX CC from the Cassava vein mosaic virus. Especially, the promoters are

XX CC derived from intergenic regions. The chimeric promoters are useful

XX CC for producing transgenic plants.

XX SQ Sequence 600 BP; 188 A; 111 C; 147 G; 154 T; 0 other;

XX Query Match 56.2%; Score 35.4; DB 21; Length 600;

XX Best Local Similarity 97.3%; Pred. No. 0.00035;

XX Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX OY 1 GCGGAAAGTACCTTATGCACTTGTGTTAC 37

XX |||||

XX DB 197 GCGGAAAGTACCTTATGCACTTGTGTTAC 233

XX RESULT 15

XX ABL79935/C

XX ID ABL79935 standard; CDNA; 434 BP.

XX AC ABL79935;

XX 17-MAY-2002 (first entry)

XX Human ovarian cancer related cDNA clone SEQ ID NO:2913.

XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.

XX XX

OS Homo sapiens.
XX
PN W0200192581-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001MO-US17756.
XX
PR 26-MAY-2000; 2000US-207484P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Algate PA, Harlocker SL, Jones R;
XX
DR WPI; 2002-122075/16.
XX
PT Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT polypeptide, antibody specific to polypeptide or T cell expressing
PT polypeptide
XX
PS Claim 1; SEQ ID 2913; 4899p; English.
XX
CC The present invention describes a composition (I) comprising: carriers
CC and immunostimulants; and a polypeptide (II) of a ovarian tumor
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to
CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
CC population of (II), or antigen presenting cells that express (II).
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
CC (S1) can be used for detecting ovarian cancer in a patient's biological
CC sample preferably serum or ovarian tissue. The method comprises
CC contacting a biological sample from a patient with (IV), detecting the
CC amount of polynucleotide hybridising to (IV) and comparing the amount to
CC a predetermined cutoff value and thereby detecting ovarian cancer in the
CC patient, where the amount of polynucleotide hybridising to (IV) is
CC detected preferably by polymerase chain reaction (PCR). (I) comprising
CC (III) and/or (II) is useful for stimulating and/or expanding T cells
CC specific for an ovarian tumor protein comprising contacting T cells
CC with (III) or (II). (III) is useful in design and preparation of
CC ribozyme molecules for inhibiting expression of the tumour polypeptides
CC and proteins in tumour cells; and to isolate a full length gene from a
CC suitable library e.g., a tumour cDNA library using well known
CC techniques.
XX
SQ Sequence 434 BP; 136 A; 66 C; 92 G; 140 T; 0 other;
XX
Query Match 39.4%; Score 24.8; DB 24; Length 434;
Best Local Similarity 63.3%; Pred. No. 5;
Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
XX
QY 4 GGAAGTACCTTATGCACTTGTACTACCGGTATGCGGATGCCAAGCTTAT 63
II III III III III III III III III III III III III III
DB 92 GGTATAGCAATGTCATTTGTTACTGGGTGTTCTGATCAAACTTCAACAGCTATAT 33

Search completed: May 24, 2003, 14:34:43
Job time : 110.726 secs

GenCore version 5.1.4.p5 4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 13:52:01 ; Search time 26.0806 Seconds
(without alignments)
740.804 Million cell updates/sec

Title: US-09-963-803-11

Perfect score: 63

Sequence: 1 ggcgggaagtaacctatgc.....tgccggtcccaacttat 63

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*

1: /cgn2.6/ptodata/1/ina/5A.COMB.seq:*

2: /cgn2.6/ptodata/1/ina/5B.COMB.seq:*

3: /cgn2.6/ptodata/1/ina/6A.COMB.seq:*

4: /cgn2.6/ptodata/1/ina/6B.COMB.seq:*

5: /cgn2.6/ptodata/1/ina/PTUS.COMB.seq:*

6: /cgn2.6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22.2	35.2	1312	4	US-09-193-792-20
C 2	22.2	35.2	1669	2	US-08-916-902A-2
C 3	22.2	35.2	1669	2	US-09-213-389-2
C 4	22.2	35.2	2021	4	US-09-193-792-2
C 5	22.2	35.2	2284	4	US-09-193-792-1
C 6	22.2	35.2	3140	4	US-08-961-527-158
C 7	21.8	34.6	6082	4	US-09-605-785-535
C 8	21.8	34.6	6082	4	US-09-439-313-535
C 9	21.8	34.6	6140	4	US-09-605-785-535
C 10	21.8	34.6	6140	4	US-09-439-313-536
C 11	21.2	33.7	3611	2	US-08-727-118-1
C 12	20.8	33.0	2233	3	US-08-680-506-4
C 13	20.8	33.0	5077	3	US-08-680-506-2
C 14	20.8	33.0	8321	3	US-08-680-506-1
C 15	20.8	33.0	12124	1	US-08-181-271A-36
C 16	20.8	33.0	12124	1	US-08-449-315-36
C 17	20.8	33.0	12124	1	US-08-444-803-36
C 18	20.8	33.0	12124	1	US-08-449-043-36
C 19	20.8	33.0	12124	1	US-08-456-265A-36
C 20	20.8	33.0	12124	1	US-08-455-416-36
C 21	20.8	33.0	12124	1	US-08-455-244-36
C 22	20.8	33.0	12124	1	US-08-454-876-36
C 23	20.8	33.0	12124	2	US-08-457-364-36
C 24	20.8	33.0	12124	2	US-08-456-262-36
C 25	20.8	33.0	12124	2	US-08-456-240-36
C 26	20.8	33.0	12124	2	US-08-455-736-36
C 27	20.8	33.0	12124	2	US-08-971-217-36

C 28	20.8	33.0	12124	4	US-09-350-600-36	Sequence 36, Appl
C 29	20.8	33.0	41708	4	US-09-470-512A-3	Sequence 3, Appl1
C 30	20.6	32.7	648	4	US-09-134-001C-458	Sequence 458, App
C 31	20.6	32.7	1275	4	US-09-134-001C-2388	Sequence 2388, App
C 32	20.6	32.7	1551	4	US-09-134-001C-567	Sequence 567, App
C 33	20.6	32.7	4223	4	US-08-845-258-7	Sequence 7, Appl1
C 34	20.6	32.7	4223	4	US-08-845-258-45	Sequence 45, Appl
C 35	20.6	32.7	4223	4	US-08-990-571-7	Sequence 7, Appl1
C 36	20.6	32.7	4223	4	US-08-990-571-45	Sequence 45, Appl
C 37	20.6	32.7	4223	4	US-08-723-142A-7	Sequence 7, Appl1
C 38	20.6	32.7	4223	4	US-08-723-142A-45	Sequence 45, Appl
C 39	20.6	32.7	4223	4	US-09-528-784A-7	Sequence 7, Appl1
C 40	20.6	32.7	4223	4	US-09-528-784A-45	Sequence 45, Appl
C 41	20.6	32.7	5912	2	US-08-629-001A-1	Sequence 1, Appl1
C 42	20.6	32.7	5912	4	US-08-642-274D-1	Sequence 1, Appl1
C 43	20.6	32.7	5912	4	US-08-952-127-1	Sequence 1, Appl1
C 44	20.6	32.7	5912	4	US-08-952-014C-1	Sequence 1, Appl1
C 45	20.6	32.7	6525	1	US-08-493-092-3	Sequence 3, Appl1

ALIGNMENTS

```
RESULT 1
US-09-193-792-20/c
: Sequence 20, Application US/09193792B
: Patent No. 6180344
: GENERAL INFORMATION:
: APPLICANT: Chen, Bin
: TITLE OF INVENTION: 5' Upstream Region Sequences of the MYO1 Gene
: FILE REFERENCE: D6015
: CURRENT APPLICATION NUMBER: US/09/193,792B
: PRIOR FILING DATE: 1998-11-17
: PRIOR APPLICATION NUMBER: US 60/065,113
: NUMBER OF SEQ ID NOS: 20
: SEQ ID NO 20
: LENGTH: 1312
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: Pcti-Ehei fragment (Pcti.3) inserted in the multiple
: OTHER INFORMATION: cloning region of a pcle enhancer vector to construct
: OTHER INFORMATION: the transfection plasmid
US-09-193-792-20
Query Match 35.2%; Score 22.2; DB 4; Length 1312;
Best Local Similarity 64.7%; Pred. No. 9.4;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
OY 11 AACCTTATGCAATTGTACTTGTTACCCGGTATCCCGGTTCCCAAGCTTT 61
Db 1091 AGCCTTAGCGCGCTGACACTTGGCTCTCCGCGACCCCTTCCAACTCT 1041
RESULT 2
US-08-916-902A-2
: Sequence 2, Application US/08916902A
: Patent No. 5871930
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Lal, Preeti
: APPLICANT: Corley, Neil C.
: TITLE OF INVENTION: HIGH AFFINITY IMMUNOGLOBULIN E
: TITLE OF INVENTION: RECEPTOR-LIKE PROTEIN
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
```

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,902A
FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0371 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAINOT04
CLONE: 927955
US-08-916-902A-2

Query Match 35.2%; Score 22.2; DB 2; Length 1669;
Best Local Similarity 61.0%; Pred. No. 10;
Matches 36; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Db 435 GGAAGTACCTTATGATTTGATCGGTATCGGGTACACATTTGGGGGTCACTATCTTAT 493

Query 5 GGAAGTACCTTATGATTTGATCGGTATCGGGTATCGGGTACACATTTGGGGGTCACTATCTTAT 63

RESULT 3
US-09-213-389-2
Sequence 2, Application US/09213389
Patent No. 5977072
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
TITLE OF INVENTION: HIGH AFFINITY IMMUNOGLOBULIN E
TITLE OF INVENTION: RECEPTOR-LIKE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/213,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,902
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0371 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAINOT04
CLONE: 927955
US-09-213-389-2

Query Match 35.2%; Score 22.2; DB 2; Length 1669;
Best Local Similarity 61.0%; Pred. No. 10;
Matches 36; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Db 435 GGAAGTACCTTATGATTTGATCGGTATCGGGTACACATTTGGGGGTCACTATCTTAT 493

Query 5 GGAAGTACCTTATGATTTGATCGGTATCGGGTATCGGGTACACATTTGGGGGTCACTATCTTAT 63

RESULT 4
US-09-193-792-2/c
Sequence 2, Application US/09193792B
Patent No. 6180344
GENERAL INFORMATION:
APPLICANT: Chen, Bin
TITLE OF INVENTION: 5' Upstream Region Sequences of the MYO1 Gene
FILE REFERENCE: D6015
CURRENT APPLICATION NUMBER: US/09/193,792B
CURRENT FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US 60/065,113
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 2
LENGTH: 2021
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: PstI fragment (PP2.0) used as a hybridization probe
US-09-193-792-2

Query Match 35.2%; Score 22.2; DB 4; Length 2021;
Best Local Similarity 64.7%; Pred. No. 10;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Db 1091 AGCCCTAGCGCGGTGACACTTGGCTCTCCGGCAGCCCTTCCAAACTCT 1041

Query 11 AACCTATGATTTGATTTGATCGGTATCGGGTATCGGGTCCCAAGCTTT 61

RESULT 5
US-09-193-792-1/c
Sequence 1, Application US/09193792B
Patent No. 6180344
GENERAL INFORMATION:
APPLICANT: Chen, Bin
TITLE OF INVENTION: 5' Upstream Region Sequences of the MYO1 Gene
FILE REFERENCE: D6015
CURRENT APPLICATION NUMBER: US/09/193,792B
CURRENT FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US 60/065,113
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 1
LENGTH: 2284

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: promoter
LOCATION: -1537..747
OTHER INFORMATION: 5' upstream promoter region of the human MYO1 gene
US-09-193-792-1

Query Match 35.2%; Score 22.2; DB 4; Length 2284;
Best Local Similarity 64.7%; Pred. No. 11;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 11 AACCTTAGCATTTGTAATGTTGATCCCGGTATGCCGTTCCCAAGCTTT 61
DB 1210 AGCCCTAGCGCGTGCACACTTGGCTCCGCGACGCCCTTTCCAAACCTCT 1160

RESULT 6
US-08-961-527-158/C
Sequence 158, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 Inch, 1.4Mb storage
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 158:
SEQUENCE CHARACTERISTICS:
LENGTH: 3140 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-158

Query Match 35.2%; Score 22.2; DB 4; Length 3140;
Best Local Similarity 64.7%; Pred. No. 12;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 3 CGGAAGTAACCTTATGATGTTGTAACCGGTATGCCGTTCC 53
DB 1897 CGAATCATAGATATATTCGTTGAACCTTGGTGACGAAGTATGGGATTC 1847

RESULT 7
US-09-605-785-535/C
Sequence 535, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 535
LENGTH: 6082
TYPE: DNA
ORGANISM: Homo sapiens
US-09-605-785-535

Query Match 34.6%; Score 21.8; DB 4; Length 6082;
Best Local Similarity 61.4%; Pred. No. 19;
Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 6 AAAGTAACCTTATGATGTTGTAACCGGTATGCCGTTCCCAACTTTA 62
DB 2431 ACAGTGACATTTAGCATTTGTTGTTGCCAGTATGAAGCACCAACTTGA 2375

RESULT 8
US-09-439-313-535/C
Sequence 535, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 535
LENGTH: 6082
TYPE: DNA
ORGANISM: Homo sapiens
US-09-439-313-535

Query Match 34.6%; Score 21.8; DB 4; Length 6082;
Best Local Similarity 61.4%; Pred. No. 19;
Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 6 AAAGTAACCTTATGATGTTGTAACCGGTATGCCGTTCCCAACTTTA 62

Db 2431 ACAGTGACATTAGCACTTTGTTGTTGCCAGTATGAAGCCACCAATCTTGA 2375

RESULT 9

US-09-605-785-536/C
Sequence 536, Application US/09605785
Patent No. 6321716

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqul
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 536
LENGTH: 6140
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (4535)
OTHER INFORMATION: n-A,T,C or G
US-09-605-785-536

Query Match 34.6%; Score 21.8; DB 4; Length 6140;
Best Local Similarity 61.4%; Pred. No. 20;
Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 6 AAGTACCTTATGCACTTTGTAAGTCCGCGATGCCGTTCCCAAGCTTTA 62

Db 2405 ACAGTGACATTAGCACTTTGTTGTTGCCAGTATGAAGCCACCAATCTTGA 2349

RESULT 10

US-09-439-313-536/C
Sequence 536, Application US/09439313
Patent No. 6323505

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqul
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 536
LENGTH: 6140
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (4535)
OTHER INFORMATION: n-A,T,C or G
US-09-439-313-536

Query Match 34.6%; Score 21.8; DB 4; Length 6140;
Best Local Similarity 61.4%; Pred. No. 20;
Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 6 AAGTACCTTATGCACTTTGTAAGTCCGCGATGCCGTTCCCAAGCTTTA 62

Db 2405 ACAGTGACATTAGCACTTTGTTGTTGCCAGTATGAAGCCACCAATCTTGA 2349

RESULT 11

US-08-727-118-1/C
Sequence 1, Application US/08727118
Patent No. 5928940

GENERAL INFORMATION:

APPLICANT: MIYAZONO, KOHEI
APPLICANT: SAMPATH, KUBER T.
TITLE OF INVENTION: NOVEL MORPHOGEN-RESPONSIVE SIGNAL
TITLE OF INVENTION: TRANSDUCER AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESS: CREATIVE BIOMOLECULES, INC.
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,118
FILING DATE: 08-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: VITO PHD, CHRISTINE C.
REGISTRATION NUMBER: 39,061
REFERENCE/DOCKET NUMBER: CRP-121 [2054/91]
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3611 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 905..1264
US-08-727-118-1

Query Match 33.7%; Score 21.2; DB 2; Length 3611;
Best Local Similarity 60.3%; Pred. No. 30;
Matches 35; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 2 GCGGAAGTAACTTATGCACTTTGTAAGTCCGCGATGCCGTTCCCAAGCT 59

Db 2267 GCAGAGAGAACCTGCTCTTCTTCGTCATAGAGACCCTGCTCCCGCTCCAAAGTT 2210

RESULT 12
US-08-680-506-4/c

; Sequence 4, Application US/08680506C

; Patent No. 6008013

; GENERAL INFORMATION:

; APPLICANT: Reynolds, Paul R.

; TITLE OF INVENTION: CHONDROCYTE PROTEINS

; FILE REFERENCE: 176/60091

; CURRENT APPLICATION NUMBER: US/08/680,506C

; CURRENT FILING DATE: 1996-07-08

; EARLIER APPLICATION NUMBER: 60/021,672

; EARLIER FILING DATE: 1996-07-05

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 4

; LENGTH: 2233

; TYPE: DNA

; ORGANISM: Gallus gallus

US-08-680-506-4

Query Match

Best Local Similarity 33.0%; Score 20.8; DB 3; Length 2233;

Best Local Similarity 70.0%; Pred. No. 38;

Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 9 GTACCTTATGCACTTGTGTAACCTGCTACCGGATGCGG 48
Db 1708 GTGGCCATGCACTTTTATTATTAGCTTCCAGAAATGCTG 1669

RESULT 13

US-08-680-506-2/c

; Sequence 2, Application US/08680506C

; Patent No. 6008013

; GENERAL INFORMATION:

; APPLICANT: Reynolds, Paul R.

; TITLE OF INVENTION: CHONDROCYTE PROTEINS

; FILE REFERENCE: 176/60091

; CURRENT APPLICATION NUMBER: US/08/680,506C

; CURRENT FILING DATE: 1996-07-08

; EARLIER APPLICATION NUMBER: 60/021,672

; EARLIER FILING DATE: 1996-07-05

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 2

; LENGTH: 5027

; TYPE: DNA

; ORGANISM: Gallus gallus

US-08-680-506-2

Query Match

Best Local Similarity 33.0%; Score 20.8; DB 3; Length 5027;

Best Local Similarity 70.0%; Pred. No. 46;

Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 9 GTACCTTATGCACTTGTGTAACCTGCTACCGGATGCGG 48
Db 1708 GTGGCCATGCACTTTTATTATTAGCTTCCAGAAATGCTG 1669

RESULT 14

US-08-680-506-1/c

; Sequence 1, Application US/08680506C

; Patent No. 6008013

; GENERAL INFORMATION:

; APPLICANT: Reynolds, Paul R.

; TITLE OF INVENTION: CHONDROCYTE PROTEINS

; FILE REFERENCE: 176/60091

; CURRENT APPLICATION NUMBER: US/08/680,506C

; CURRENT FILING DATE: 1996-07-08

; EARLIER APPLICATION NUMBER: 60/021,672

; EARLIER FILING DATE: 1996-07-05

; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8321
; TYPE: DNA
; ORGANISM: Gallus gallus
US-08-680-506-1

Query Match 33.0%; Score 20.8; DB 3; Length 8321;
Best Local Similarity 70.0%; Pred. No. 52;

Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 9 GTACCTTATGCACTTGTGTAACCTGCTACCGGATGCGG 48
Db 4622 GTGGCCATGCACTTTTATTATTAGCTTCCAGAAATGCTG 4583

RESULT 15

US-08-181-271A-36/c

; Sequence 36, Application US/08181271A

; Patent No. 5614395

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.

; APPLICANT: Harms, Christian

; APPLICANT: Melns, Jr., Frederick

; APPLICANT: Montoya, Alice

; APPLICANT: Moyer, Mary B.

; APPLICANT: Neuhaus, Jean-Marc

; APPLICANT: Payne, George B.

; APPLICANT: Sperison, Christoph

; APPLICANT: Stinson, Jeffrey R.

; APPLICANT: Uknes, Scott J.

; APPLICANT: Ward, Eric R.

; APPLICANT: Williams, Shericca C.

; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: New York

COUNTRY: USA

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/181,271A

FILING DATE: 13-JAN-94

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/093,301

FILING DATE: 16-JUL-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/937,197

FILING DATE: 6-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/678,378

FILING DATE: 1-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566

FILING DATE: 6-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/165,667

FILING DATE: 8-MAR-1988

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: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/042,847
: FILING DATE: 6-APR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/632,441
: FILING DATE: 21-DEC-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/425,504
: FILING DATE: 20-OCT-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/848,506
: FILING DATE: 6-MAR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/768,122
: FILING DATE: 27-SEP-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/580,431
: FILING DATE: 7-SEP-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/368,672
: FILING DATE: 20-JUN-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/329,018
: FILING DATE: 24-MAR-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/045,957
: FILING DATE: 12-APR-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Elmer, James Scott
: REGISTRATION NUMBER: 36,129
: REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919)541-8614
: TELEFAX: (919)541-8689
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 12124 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: ORGANISM: Cucumis sativus
: INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
: IMMEDIATE SOURCE:
: CLONE: pBScucchrht5
:
: US-08-181-271A-36

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Query Match 33.0%; Score 20.8; DB 1; Length 12124;
Best Local Similarity 70.0%; Pred. No. 37;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 23 TTGTAACTTGTTACCGGTATCCGGTTCCTCAAGCTTTA 62
||| ||||| ||| ||||| |||||
DB 8248 TTGGAAGTTGTGACGCGGCTCCGTTGAGAAAGCTGTA 8209

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Search completed: May 24, 2003, 15:37:41
 Job time : 32.0806 secs

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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 13:48:31 ; Search time 49.1129 Seconds

(without alignments)
1693.834 Million cell updates/sec

Title: US-09-963-803-11

Perfect score: 63

Sequence: 1 ggcggaagtaacctatgc.....tgccggttcccaactttat 63

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Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 660231138 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEM_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEM_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	100.0	63	US-09-963-803-11	Sequence 11, Appl
2	63	100.0	317	US-09-963-803-3	Sequence 3, Appl
3	63	100.0	371	US-09-963-803-5	Sequence 5, Appl
4	61.4	97.5	301	US-09-963-803-7	Sequence 7, Appl
5	61.4	97.5	348	US-09-963-803-4	Sequence 4, Appl
6	61.4	97.5	398	US-09-963-803-6	Sequence 6, Appl
7	42	66.7	243	US-09-963-803-1	Sequence 1, Appl
8	41.2	65.4	392	US-09-963-803-21	Sequence 21, Appl
9	38.8	61.6	604	US-09-963-803-23	Sequence 23, Appl
10	37	58.7	472	US-09-963-803-25	Sequence 25, Appl
11	37	58.7	541	US-09-963-803-24	Sequence 24, Appl
12	35.4	56.2	393	US-09-963-803-19	Sequence 19, Appl
13	35.4	56.2	462	US-09-963-803-20	Sequence 20, Appl
14	35.4	56.2	600	US-09-963-803-22	Sequence 22, Appl
15	24.8	39.4	434	US-09-867-701-2913	Sequence 2913, Ap
16	24.8	39.4	539	US-09-736-457-148	Sequence 148, App
17	24.8	39.4	539	US-09-902-941-148	Sequence 148, App
18	24.8	39.4	539	US-09-849-626-148	Sequence 148, App
19	24.8	39.4	539	US-10-017-754-148	Sequence 148, App

c	20	23.2	36.8	2241	9	US-09-938-842A-646	Sequence 646, App
c	21	22.6	35.9	424	10	US-09-983-965-762	Sequence 762, App
c	22	22.4	35.6	347	10	US-09-867-701-5603	Sequence 5603, App
c	23	22.4	35.6	12010	10	US-09-880-107-3369	Sequence 3369, App
c	24	22.4	35.6	83450	9	US-09-811-469-3	Sequence 3, Appl
c	25	22.2	35.2	771	10	US-09-974-300-2855	Sequence 2855, App
c	26	22.2	35.2	1563	10	US-09-765-705-21	Sequence 21, Appl
c	27	22.2	35.2	2438	9	US-09-832-846-227	Sequence 227, App
c	28	22.2	35.2	684973	10	US-09-263-959-1	Sequence 1, Appl
c	29	22	34.9	744	10	US-09-833-381-293	Sequence 293, App
c	30	22	34.9	1936	10	US-09-880-107-3832	Sequence 3832, App
c	31	22	34.9	6558	10	US-09-764-877-3503	Sequence 3503, App
c	32	21.8	34.6	1427	10	US-09-925-300-613	Sequence 613, App
c	33	21.8	34.6	3786	9	US-10-012-896-1006	Sequence 1006, App
c	34	21.8	34.6	4395	9	US-10-012-896-1007	Sequence 1007, App
c	35	21.8	34.6	6082	9	US-10-012-896-535	Sequence 535, App
c	36	21.8	34.6	6082	9	US-09-895-793-535	Sequence 535, App
c	37	21.8	34.6	6082	9	US-09-895-814-535	Sequence 535, App
c	38	21.8	34.6	6082	9	US-10-010-940-535	Sequence 535, App
c	39	21.8	34.6	6082	10	US-09-759-143-535	Sequence 535, App
c	40	21.8	34.6	6082	10	US-09-780-669-535	Sequence 535, App
c	41	21.8	34.6	6082	10	US-09-822-827-535	Sequence 535, App
c	42	21.8	34.6	6140	9	US-10-012-896-536	Sequence 536, App
c	43	21.8	34.6	6140	9	US-09-895-793-536	Sequence 536, App
c	44	21.8	34.6	6140	9	US-09-895-814-536	Sequence 536, App
c	45	21.8	34.6	6140	9	US-10-010-940-536	Sequence 536, App

ALIGNMENTS

RESULT 1
US-09-963-803-11
Sequence 11, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yello
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963, 803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 63
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: S4
US-09-963-803-11
Query Match 100.0%; Score 63; DB 9; Length 63;
Best Local Similarity 100.0%; Pred. No. 1; 1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCGGAAAGTAACTTATGCAATTTGTAACCTGCTAACCCGGATGCCGTTCCCAAGCTT 60
DB 1 GCGGAAAGTAACTTATGCAATTTGTAACCTGCTAACCCGGATGCCGTTCCCAAGCTT 60
OY 61 TAT 63
DB 61 TAT 63
RESULT 2
US-09-963-803-3
Sequence 3, Application US/09963803

Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 317
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter MPr1116
NAME/KEY: promoter
LOCATION: (1)..(317)
OTHER INFORMATION:
US-09-963-803-3

Query Match 100.0%; Score 63; DB 9; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGGAAGTAACCTTATGATTTGTAACTGGTATGCCGCTATGCCGTTCCCAAGCTT 60
DB 195 GGGGGAAGTAACCTTATGATTTGTAACTGGTATGCCGCTATGCCGTTCCCAAGCTT 254

QY 61 TAT 63
DB 255 TAT 257

RESULT 3
US-09-963-803-5
Sequence 5, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 371
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter MPr1146
NAME/KEY: promoter
LOCATION: (1)..(371)
OTHER INFORMATION:
US-09-963-803-5

Query Match 100.0%; Score 63; DB 9; Length 371;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGGAAGTAACCTTATGATTTGTAACTGGTATGCCGCTATGCCGTTCCCAAGCTT 60

DB 249 GGGGGAAGTAACCTTATGATTTGTAACTGGTATGCCGCTATGCCGTTCCCAAGCTT 308
QY 61 TAT 63
DB 309 TAT 311

RESULT 4
US-09-963-803-7
Sequence 7, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 301
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter MPr1154
NAME/KEY: promoter
LOCATION: (1)..(301)
OTHER INFORMATION:
US-09-963-803-7

Query Match 97.5%; Score 61.4; DB 9; Length 301;
Best Local Similarity 98.4%; Pred. No. 8.1e-15;
Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGGAAGTAACCTTATGATTTGTAACTGGTATGCCGCTATGCCGTTCCCAAGCTT 60
DB 181 GGGGGAAGTAACCTTATGATTTGTAACTGGTATGCCGCTATGCCGTTCCCAAGCTT 240

QY 61 TAT 63
DB 241 TAT 243

RESULT 5
US-09-963-803-4
Sequence 4, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 348
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter MPr1117

Query Match 100.0%; Score 63; DB 9; Length 348;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGGAAGTAACCTTATGATTTGTAACTGGTATGCCGCTATGCCGTTCCCAAGCTT 60

FEATURE:
NAME/KEY: Promoter
LOCATION: (1)..(348)
OTHER INFORMATION:
US-09-963-803-4

Query Match
Best Local Similarity 97.5%; Score 61.4; DB 9; Length 348;
Pred. No. 8.5e-15;
Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGGAAAGTACCTTATGCTTGTGTAACCTTGTTACCCGGTATGCCGTTCCCAAGCTT 60
|||||
DB 228 GCGGAAAGTACCTTATGCTTGTGTAACCTTGTTACCCGGTATGCCGTTCCCAAGCTT 287

QY 61 TAT 63
|||
DB 288 TAT 290

RESULT 6
US-09-963-803-6

Sequence 6, Application US/09963803
Publication No. US20030028922A1

GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1

SEQ ID NO 6
LENGTH: 398
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter MP1147
NAME/KEY: Promoter
LOCATION: (1)..(398)
OTHER INFORMATION:
US-09-963-803-6

Query Match
Best Local Similarity 97.5%; Score 61.4; DB 9; Length 398;
Pred. No. 8.9e-15;
Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGGAAAGTACCTTATGCTTGTGTAACCTTGTTACCCGGTATGCCGTTCCCAAGCTT 60
|||||
DB 278 GCGGAAAGTACCTTATGCTTGTGTAACCTTGTTACCCGGTATGCCGTTCCCAAGCTT 337

QY 61 TAT 63
|||
DB 338 TAT 340

RESULT 7
US-09-963-803-1

Sequence 1, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925

US-09-963-803-1
Sequence 1, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925

PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 243
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 243 bp Fragment from the intergenic region of commelina yellow
OTHER INFORMATION: title virus

Query Match
Best Local Similarity 66.7%; Score 42; DB 9; Length 243;
Pred. No. 4.1e-07;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TTTGTAAGTGTGTTACCCGGTATGCCGTTCCCAAGCTTAT 63
|||||
DB 153 TTTGTAAGTGTGTTACCCGGTATGCCGTTCCCAAGCTTAT 194

QY 61 TAT 62
|||
DB 257 TAT 258

RESULT 8
US-09-963-803-21

Sequence 21, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 392
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter MP1164
NAME/KEY: Promoter
LOCATION: (1)..(392)
OTHER INFORMATION:
US-09-963-803-21

Query Match
Best Local Similarity 65.4%; Score 41.2; DB 9; Length 392;
Pred. No. 1e-06;
Matches 49; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 GCGGAAAGTACCTTATGCTTGTGTAACCTTGTTACCCGGTATGCCGTTCCCAAGCTT 60
|||||
DB 197 GCGGAAAGTACCTTATGCTTGTGTAACCTTGTTACCCGGTATGCCGTTCCCAAGCTT 256

QY 61 TAT 62
|||
DB 257 TAT 258

RESULT 9
US-09-963-803-23

Sequence 23, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925

US-09-963-803-23
Sequence 23, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925

GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
PRIORITY FILING DATE: 2001-09-26
PRIORITY FILING DATE: 1999-03-29
PRIORITY FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 23
LENGTH: 604
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: promoter MPr1167
NAME/KEY: promoter
LOCATION: (1)..(604)
OTHER INFORMATION:
US-09-963-803-23

Query Match 61.6%; Score 38.8; DB 9; Length 604;
Best Local Similarity 95.2%; Pred. No. 1e-05;
Matches 40; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GCGGAAAGTAACCTTATGCACTTGTACTGTTACCGGT 42
Db 278 GCGGAAAGTAACCTTATGCACTTGTACTGTTACCT 319

RESULT 10
US-09-963-803-25
Sequence 25, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
PRIORITY FILING DATE: 2001-09-26
PRIORITY FILING DATE: 1999-03-29
PRIORITY FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 25
LENGTH: 472
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: promoter MPr1169
NAME/KEY: promoter
LOCATION: (1)..(472)
OTHER INFORMATION:
US-09-963-803-25

Query Match 58.7%; Score 37; DB 9; Length 472;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGGAAAGTAACCTTATGCACTTGTACTGTTAC 37
Db 278 GCGGAAAGTAACCTTATGCACTTGTACTGTTAC 314

RESULT 11

US-09-963-803-24
Sequence 24, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
PRIORITY FILING DATE: 2001-09-26
PRIORITY FILING DATE: 1999-03-29
PRIORITY FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 24
LENGTH: 541
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: promoter MPr1168
NAME/KEY: promoter
LOCATION: (1)..(541)
OTHER INFORMATION:
US-09-963-803-24

Query Match 58.7%; Score 37; DB 9; Length 541;
Best Local Similarity 100.0%; Pred. No. 5.2e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGGAAAGTAACCTTATGCACTTGTACTGTTAC 37
Db 278 GCGGAAAGTAACCTTATGCACTTGTACTGTTAC 314

RESULT 12
US-09-963-803-19
Sequence 19, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
PRIORITY FILING DATE: 2001-09-26
PRIORITY FILING DATE: 1999-03-29
PRIORITY FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 19
LENGTH: 393
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: promoter MPr1162
NAME/KEY: promoter
LOCATION: (1)..(393)
OTHER INFORMATION:
US-09-963-803-19

Query Match 56.2%; Score 35.4; DB 9; Length 393;
Best Local Similarity 97.3%; Pred. No. 0.0002;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCGGAAAGTAACCTTATGCACTTGTACTGTTAC 37
Db 197 GCGGAAAGTAACCTTATGCACTTGTACTGTTAC 233

RESULT 13

US-09-963-803-20
; Sequence 20, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; TITLE OF INVENTION: vitus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1163
; FEATURE:
; NAME/KEY: Promoter
; LOCATION: (1)..(462)
; OTHER INFORMATION:
US-09-963-803-20

Query Match

Best Local Similarity 56.2%; Score 35.4; DB 9; Length 462;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGGGAAGTACCTTATGCACTTGTACTTGTTAC 37
DB 197 GCGGGAAGTACCTTATGCACTTGTACTTGTTAC 233

RESULT 14

US-09-963-803-22
; Sequence 22, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; TITLE OF INVENTION: vitus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MPr1165
; FEATURE:
; NAME/KEY: Promoter
; LOCATION: (1)..(600)
; OTHER INFORMATION:
US-09-963-803-22

Query Match 56.2%; Score 35.4; DB 9; Length 600;
Best Local Similarity 97.3%; Pred. No. 0.00024;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGGGAAGTACCTTATGCACTTGTACTTGTTAC 37
DB 197 GCGGGAAGTACCTTATGCACTTGTACTTGTTAC 233

RESULT 15

US-09-867-701-2913/c
; Sequence 2913, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Agiate, Paul A.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.487
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2913
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-2913

Query Match 39.4%; Score 24.8; DB 10; Length 434;
Best Local Similarity 63.3%; Pred. No. 3.5;
Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 4 GGAAGTACCTTATGCACTTGTACTTGTTACCGGTTCCCAAGCTTAT 63
DB 92 GGAAGTACCTTATGCACTTGTACTTGTTACCGGTTCCCAAGCTTAT 33

Search completed: May 24, 2003, 15:36:01
Job time : 51.1129 secs

Query Match	41.98;	Score 26.4;	DB 17;	Length 501;
Best Local Similarly	65.08;	Pred. No. 9.6;		
Matches 39; Conservative	0;	Mismatches 21;	Indels 0;	Gaps 0;

DEFINITION	024_O_09-21 SmbAC1 Schistosoma mansoni genomic clone 024O09 5', DNA sequence.
ACCESSION	BH183804

KEYWORDS	GSS.
SOURCE	Schistosoma mansoni.
ORGANISM	Schistosoma mansoni.
REFERENCE	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
AUTHORS	Strigoidida; Schistosomatidae; Schistosomatidae; Schistosoma.
TITLE	1 (bases 1 to 835)
JOURNAL	le Paslier, M.-C., Pierce, R.J., Merlín, F., Hiral, H., Wu, W., Williams
MEDLINE	, D.L., Johnston, D., Loyverde, P.T. and le Paslier, D.
COMMENT	Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library Genomics 65 (2), 87-94 (2000) 20247247 Other_GSSes: 024-Q-09-rev Contact: Pierce RJ INSERM U 167 Institut Pasteur de Lille 1 rue du Professeur A. Calmette, 59019-Lille, France Tel: (33) (0)3 20877783 Fax: (33) (0)3 20877888 Email: Raymond.Pierce@pasteur-lille.fr CNS sequencing ID=DS0AA024AH05CPI Plate: 024 row: 0 column: 09 Seq primer: M13 -21 primer Class: BAC ends High quality sequence stop: 835.
FEATURES	Location/Qualifiers
source	1..835
	/organism="Schistosoma mansoni"
	/strain="Puerto-Rican"
	/db_xref="taxon:6183"
	/clone="024009"
	/clone_lib="SmbAC1"
	/sex="mixed"
	/dev_stage="cercariae"
	/lab_host="Biomphalaria glabrata"
	/note="Vector: pBlotAC 11; Site_1: Hind III; Partially Hind III digested and size-selected S. mansoni cercarial DNA was ligated into Hind III digested pBlotAC 11 vector and used to transform E. coli DH10B. The complete library contains 23808 clones from 4 independent sizing-ligation-transformations. Average insert size ranges from 70-127 kb and genome coverage is 7.9-fold."
BASE COUNT	273 a 147 c 141 g 261 t 13 others
ORIGIN	
Query Match	39.7%; Score 25; DB 17; Length 835;
Best Local Similarity	75.6%; Pred. No. 39;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	
0y	6 AAGTACCTTATGATTTGATCTGTTACCTGTTACCGCGTATGC 46
Db	69 AAGTCACTTATGCTTTTCACCACTGATTCGCGTTATTC 109
RESULT 5	
CNS070W0	835 bp DNA linear GSS 10-OCT-2001
LOCUS	T7 end of clone 024AH05 of library SmbAC1 from strain Puerto-Rican
DEFINITION	of Schistosoma mansoni, genomic survey sequence.
ACCESSION	AL620754
VERSION	AL620754.1 GI:16034896
KEYWORDS	GSS.
SOURCE	Schistosoma mansoni.
ORGANISM	Schistosoma mansoni.
REFERENCE	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
AUTHORS	Strigoidida; Schistosomatidae; Schistosomatidae; Schistosoma.
TITLE	1 (bases 1 to 835)
JOURNAL	le Paslier, M.-C., Pierce, R.J., Merlín, F., Hiral, H., Wu, W., Williams
MEDLINE	, D.L., Johnston, D., Loyverde, P.T. and le Paslier, D.
COMMENT	Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library Genomics 65 (2), 87-94 (2000) 20247247

```

PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
SOURCE
10783255
2 (bases 1 to 835)
Genoscope.
Direct Submission
Submitted (05-OCT-2001) Genoscope - Centre National de Sequencage :
BP 191.91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
Partially Hind III digested and size-selected S. mansoni cercarial
DNA was ligated into Hind III digested pBelO8AC 11 vector and used
to transform E. coli DH10B. The complete library contains 23808
clones from 4 independent sizing-ligation-transformations. Average
insert size ranges from 70-1127 kb and genome coverage is 7.9-fold.
location/qualifiers
1..835
/organism="Schistosoma mansoni"
/strain="Puerto-Rican"
/db_xref="taxon:6183"
/clone="024AH05"
/clone_lib="SmBAC1"
/notes="End : T7"
BASE COUNT 273 a 147 c 141 g 261 t 13 others
ORIGIN
Query Match 39.7%; Score 25; DB 17; Length 835;
Best Local Similarity 75.6%; Pred. NO. 39;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Oy 6 AAGATACCTTATGCATTGTACTGTTACCTGGTACCGGTATGC 46
||||| ||||| ||||| ||||| ||||| |||||
Db 69 AAGTCACTTATATGCTTTTCAACCTGATTCACGCTATTC 109
RESULT 6
R54659 426 bp mRNA linear EST 22-MAY-1995
DEFINITION Y174607 r1 Soares breast 2NbHst Homo sapiens cDNA clone
LOCUS R54659
IMAGE:154477 5', mRNA sequence.
ACCESSION R54659
VERSION R54659.1 GI:819051
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 426)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rikkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaethis,E., Waterston
,R., Williams,A., Wohlmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel.: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 721
High quality sequence stops: 315 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 721 Std Error: 0.00
Seq primer: M13Rpl
High quality sequence stop: 315.
location/qualifiers
1..426
/organism="Homo sapiens"
/db_xref="GDB:566912"
/db_xref="taxon:9606"
/clone="IMAGE:154477"
/clone_lib="Soares breast 2NbHst"
/sex="Female"
/dev_stage="adult"
FEATURES
SOURCE
1..426
/organism="Homo sapiens"
/db_xref="GDB:566912"
/db_xref="taxon:9606"
/clone="IMAGE:154477"
/clone_lib="Soares breast 2NbHst"
/sex="Female"
/dev_stage="adult"

```

```

/lab.host="DH10B (ampicillin resistant)"
/notice="Organ. breast; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGACAGTGGAGCGGCCCGCTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of a modified pT73 vector (Pharmacia).
Library went through one round of normalization to a Cot
230. Library constructed by Bento Soares and M.Fátima
Bonaldo."

```

Query Match	39.48	Score 24, 8	DB 14	Length 426
Best Local Similarity	63.38	Pred. No. 39		
Matches 38; Conservative	0	Mismatches 22	Indels 0	Gaps 0

```

0y      4 GGAAAGTACCTTATGCATTGTTAACCGGTATGCCGTTCACAAGCTTAT 63
        ||| |||| | | | | | | | | | | | | | | | | | | | |
db     284 GGTAAACMACTTGTCATTGTTACTCGGGTCTTAGATCAAACTTCACAAGCTTAT 225

```

RESULT	7
AA291914/c	
LOCUS	
DEFINITION	434 bp mRNA linear EST 16-MAY-1997
	ZC39G01.r1 Soares tumor NBH07 Homo sapiens CDNA clone IMAGE:724752 5', mRNA sequence.

ACCESSION	AA291914	GI:1939892
VERSION	AA291914.1	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
1 (bases 1 to 434)

TITLE
JOURNAL
COMMENT

Kucaba, T., Lacy, M., Le, N., Lennon, G., Maria, M., Martin, J., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie,
, T., Waterston, R., and Wilson, R.
Mashu-merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK

Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LINTL; contact the
 IMAGE Consortium (info@image.limn.gov) for further information.
 Seq primer: 28m3 rev2 Et from Amersham
 High quality sequence stop: 338.
 Location/Qualifiers
 1..434

```
BASE COUNT      136 a          66 c          92 g          140 t
ORIGIN
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="724752"
/clone_lib="Scares ovary tumor NbHOT"
/sex="Female"
/tissue_type="Ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pUT7D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTCACCAATCTGAAGTGCGAGCGCCGCGGTCTTTTCTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pUT73 vector (Pharmacia). Library constructed by Bento Soares and M.Felina Donaldso."

```

Query Match	39.48	Score	24.8	DB	9	Length	434
Best Local Similarity	63.38	Pred. No.	39				
Matches	38	Conservative	0	Mismatches	22	Indels	0
						Gaps	0

Oy 4 GGAAGTAACTATGACATTGTGTAACCTGGTATCCCGTTCCAAGCTTAA 63
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 92 GGTAAGCAACATTGTTCATTGTACTGGGTCTTAGATCAAACTTCAACAAGCATATA 330

RESULT 8	
AA290875/c	
LOCUS	493 bp mRNA linear EST 15-AUG-1997
DEFINITION	zs44dd5.r1 NCI_GCAP_GCB1 Homo sapiens CDNA clone IMAGE:700329 5', mRNA sequence.
ACCESSION	U000075

ACCESSION	AA290873	GI:19387699
VERSION	AA290875.1	
KEYWORDS	EST.	
SOURCE	human.	

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 493)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapsb@email.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information
Insert Length: 1138 Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 435.

FEATURES
source

```

/organism="Homo sapiens"
/db_xref="GDB:5739753"
/db_xref="taxon:9606"
/cdb_image="700329"
/clone_1lb="NCI_CGAP_GCH1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/notice="Vector: pUT7D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGATGAGGAGGCGCCCTCATTTTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pUT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

```

Query Match	39.4%	Score 24.8;	DB 9;	Length 493;
Best Local Similarity	63.3%;	Pred. No. 41;		
Matches 38;	Conservative 0;	Mismatches 22;	Indels 0;	Caps 0;

[illegible]

RESULT 9	LOCUS	DEFINITION	ACCESSION
Bg150109	519 bp	mRNA	EST 05-FEB-2001
Bg150109	519 bp	mRNA	linear
ncd51504.x1	NCI_CGAP_Lu24	Homo sapiens	CDNA clone
IMAGE:3407047	3'		
Bg150109		mRNA sequence.	
Bg150109			

VERSION BG150109.1 GI:12662139
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 519)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL, send email to:
 info@image.llnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 483.
 Location/Qualifiers
 1. 519
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3407047"
 /clone_1lb="NCI-CGAP_Lu24"
 /tissue_type="carcinoid"
 /lab_host="DH10B"
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; Plasmid DNA from the normalized
 library NCI CGAP Lu5 was prepared, and ss circles were
 used as tracer in a subtractive hybridization reaction.
 The driver was PCR-amplified cDNAs from a pool of 5,000
 clones made from the same library (cloneids
 1414920-1417991 and 1520904-1522439). Subtraction by Bento
 Soares and M. Fatima Bonaldo."
 BASE COUNT 180 a 106 c 81 g 152 t
 ORIGIN
 Query Match 39.4%; Score 24.8; DB 12; Length 519;
 Best Local Similarity 63.3%; Pred. No. 41;
 Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
 Oy 4 GGAAGTAACTTATGCTTGTACCTGCTACCCGCTATGCCGTTCCCACTTAT 63
 Db 452 GGTAAAGCAACATTTGTTACTGCTGTCTAGATCAACACTTCAACACTATAT 511
 RESULT 10 554 bp mRNA linear EST 08-MAR-2000
 A1970488
 LOCUS A1970488
 DEFINITION w993605.x1 NCI-CGAP CG6 Homo sapiens CDNA clone IMAGE:2479616 3'
 similar to contains Alu repetitive element; mRNA sequence.
 ACCESSION A1970488
 VERSION A1970488.1 GI:5767314
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 554)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 www-bio.llnl.gov/bdrp/image/image.html
 Insert Length: 613 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 457.
 Location/Qualifiers
 1. 554
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2479616"
 /clone_1lb="NCI-CGAP CG6"
 /tissue_type="pooled gemm cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
 from the normalized library NCI CGAP GC4 was prepared, and
 ss circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (cloneids
 1257096-1258631, 1469064-1470983, and 1475592-1476743).
 Subtraction by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 190 a 111 c 89 g 163 t 1 others
 ORIGIN
 Query Match 39.4%; Score 24.8; DB 9; Length 554;
 Best Local Similarity 63.3%; Pred. No. 42;
 Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
 Oy 4 GGAAGTAACTTATGCTTGTACCTGCTACCCGCTATGCCGTTCCCACTTAT 63
 Db 450 GGTAAAGCAACATTTGTTACTGCTGTCTAGATCAACACTTCAACACTATAT 509
 RESULT 11 730 bp mRNA linear EST 01-JUN-2000
 A9965172
 LOCUS A9965172
 DEFINITION EST377245 MAGE resequences, MAGI Homo sapiens CDNA, mRNA sequence.
 ACCESSION A9965172
 VERSION A9965172.1 GI:8155008
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 730)
 Hegde, P., Ol, R., Abernathy, K., Dharp, S., Gaspar, R., Gay, C., Holt
 I.E., Sreed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
 Quackenbush, J.
 Assessment of gene expression patterns in a model of colon tumor
 metastasis using a 19,200 element CDNA microarray
 Unpublished (2000)
 JOURNAL Contact: John Quackenbush
 COMMENT The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnq@ligr.org
 Plate: 211
 Seq primer: Forward.
 Location/Qualifiers
 1. 730
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1lb="MAGE resequences, MAGI"
 /note="Vector: BluescriptSKM"
 BASE COUNT 255 a 135 c 112 g 228 t
 ORIGIN

Query Match		39.4%	Score 24.8;	DB 10;	Length 730;	
Best Local Similarity		63.3%	Pred. No. 46;			
Matches	38;	Conservative	0;	Mismatches	22; Indels	0; Gaps

OY	4	GGAAGTAACCTTATGCAATTGTACTGTTAACCCTGGATGCCGTTCCAGCCTTAT	63
Db	448	GGAAGCAACAATGTCATTGTCTACTGGTGCTGTATAGATCAAACCTTCACAAGCTATAT	507

RESULT 12						
LOCUS	Bf107114/c		811 bp.	mRNA	linear	EST 19-OCT-2000
DEFINITION	601823675F1 NIH_MGC_79 Homo sapiens CDNA clone IMAGE:4043514 5',					
ACCESSION	Bf107114					
VERSION	Bf107114					
KEYWORDS	EST.					
SOURCE	Bf107114.1 GI:10889555					
ORGANISM	human.					
REFERENCE	Homo sapiens					
AUTHORS	Xenokryta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
JOURNAL	NIH-MGC http://mhc.ncl.nih.gov/.					
COMMENT	Unpublished (1999)					
	Contact: Robert Strausberg, Ph.D.					
	Email: cgaabs@mail.nih.gov					
	Tissue Procurement: CLONTECH Laboratories, Inc.					
	cDNA Library Preparation: CLONTECH Laboratories, Inc.					
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)					
	DNA Sequencing by: Incyte Genomics, Inc.					
	Clone distribution: MGC clone distribution information can be					
	found through the I.M.A.G.E. Consortium/LLNL at:					
	http://image.llnl.gov					
	Plate: LHC866 Row: e Column: 19					
	High quality sequence stop: 340.					
FEATURES	Location/Qualifiers					
SOURCE	1..811					
	/organism="Homo sapiens"					
	/db_xref="taxon:9606"					
	/clone="IMAGE:4043514"					
	/clone_id="NIH_MGC_79"					
	/lab_host="DH10B (TI phage-resistant)"					
	/note="Organ (placenta); Vector: pDNR-LIB (Clontech);					
	Site.1: Sfil (ggccatcgcc); Site.2: Sfil (ggccatcgcc					
	adaptor Sequence: 5'-CACGGCATATGCGC-3' and 3' adaptor					
	sequence: 5'-ATTCTAGAGCGCGGCGGCAGCATG-dt(30)BN-3'					
	(where B = A, C, or G and N = A, C, G, or T). Average					
	insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies					
	contained inserts by PCR. This library was enriched for					
	full-length clones and was constructed by Clontech					
	Laboratories (Palo Alto, CA). Note: this is a NIH_MGC					
	Library."					
BASE COUNT	240 a 159 c 153 g 259 t					
ORIGIN						
Query Match		39.4%	Score 24.8;	DB 12;	Length 811;	
Best Local Similarity		63.3%	Pred. No. 47;			
Matches	38;	Conservative	0;	Mismatches	22; Indels	0; Gaps

OY	4	GGAAGTAACCTTATGCAATTGTACTGTTAACCCTGGATGCCGTTCCAGCCTTAT	63
Db	394	GGAAGCAACAATGTCATTGTCTACTGGTGCTGTATAGATCAAACCTTCACAAGCTATAT	335

RESULT 13						
LOCUS	Bf970066/c		918 bp.	mRNA	linear	EST 22-JAN-2001
DEFINITION	6022272333F1 NIH_MGC_84 Homo sapiens CDNA clone IMAGE:4360233 5',					
ACCESSION	Bf970066					

VERSION	BF970066.1	GI:12337281
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE	1 (bases 1 to 918)	
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .	
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: L1AM10001 row: b column: 10 High quality sequence stop: 690. Location/Qualifiers 1..918 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_image:4360233" /clone_id="NIH_MGC_84" /clone_type="adrenal cortex carcinoma, cell line" /lab_host="DH10B (phage-resistant)" /note="Organ: adrenal gland; Vector: PCWV-SPORT6; Site:1; Not1, Site:2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."	
BASE COUNT	269 a	171 c 173 g 305 t
ORIGIN		
Query Match	39.4%	Score 24.8; DB 12; Length 918;
Best Local Similarity	63.3%	Pred. No. 49;
Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;		
OY	4	GGAAGTAAACCTTATGACATTTGTACTTGGTTACCGGTATGCGGTGCCAGCTTAT 63
Db	598	GGTAGCAACATTTGTTCTATTTGTTACTGTGGTCTTCTATATCAACCTTCACAGCTATAT 539
RESULT 14		
AZ315498/C	487 bp	DNA linear GSS 29-SEP-2000
LOCUS	1M0032D15R	Mouse 10kb plasmid U06C1M library Mus musculus genomic
DEFINITION	clone U06C1M0032D15 R, DNA sequence.	
ACCESSION	AZ315498	
VERSION	AZ315498.1	GI:10362388
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
TITLE	1 (bases 1 to 487)	
JOURNAL	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,	
COMMENT	Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly	
	, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.	
	and Wright, D., Weiss, R.	
	Mouse whole genome scaffolding with paired end reads from 10kb	
	plasmid inserts	
	Unpublished (2000)	
	Contact: Robert B. Weiss	
	University of Utah Genome Center	
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT	
	84112, USA	
	Tel.: 801 585 5606	
	Fax: 801 585 7177.	

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 10:21:51 ; Search time 350.903 Seconds

(Without alignments)
5225.021 Million cell updates/sec

Title: US-09-963-803-13

Perfect score: 63

Sequence: 1 catgctgcagactgactgact.....aaggatgacgactgact 63

Scoring table:

IDENTITY_NNC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htg_mus: *
34: em_htg_pln: *
35: em_htg_rnd: *
36: em_htg_man: *
37: em_htg_vit: *
38: em_sy: *
39: em_htgo_hum: *
40: em_htgo_mus: *
41: em_htgo_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	63	6 AX036610	AX036610 Sequence
2	63	100.0	63	6 AX036747	AX036747 Sequence
3	59	93.7	280	6 AX036601	AX036601 Sequence
4	59	93.7	301	6 AX036741	AX036741 Sequence
5	59	93.7	398	6 AX036740	AX036740 Sequence
6	59	93.7	472	6 AX036759	AX036759 Sequence
7	59	93.7	541	6 AX036758	AX036758 Sequence
8	59	93.7	604	6 AX036757	AX036757 Sequence
9	46	73.0	79	6 AX036611	AX036611 Sequence
10	46	73.0	259	6 AX036748	AX036748 Sequence
11	46	73.0	296	6 AX036616	AX036616 Sequence
12	46	73.0	371	6 AX036603	AX036603 Sequence
13	46	73.0	371	6 AX036739	AX036739 Sequence
14	45	71.4	392	6 AX036755	AX036755 Sequence
15	45	71.4	393	6 AX036753	AX036753 Sequence
16	45	71.4	462	6 AX036754	AX036754 Sequence
17	45	71.4	600	6 AX036756	AX036756 Sequence
18	45	71.4	9285	6 AX093047	AX093047 Sequence
19	45	71.4	15077	6 AX093052	AX093052 Sequence
20	43.4	68.9	174	8 AF434749	AF434749 Zea mays
21	43.4	68.9	189	8 AF164073	AF164073 Sequence
22	43.4	68.9	197	8 AF434747	AF434747 Zea mays
23	43.4	68.9	199	8 AF434746	AF434746 Zea mays
24	43.4	68.9	199	8 AF434748	AF434748 Zea mays
25	43.4	68.9	199	8 AF434750	AF434750 Zea mays
26	43.4	68.9	240	6 AX033493	AX033493 Sequence
27	43.4	68.9	309	6 AX044092	AX044092 Sequence
28	43.4	68.9	309	6 AX405116	AX405116 Sequence
29	43.4	68.9	331	6 BD001990	BD001990 A transge
30	43.4	68.9	332	6 E01311	E01311 Cauliflower
31	43.4	68.9	333	6 104847	104847 Sequence 3
32	43.4	68.9	354	12 ARCAMVPR	X04879 CAMV promot
33	43.4	68.9	390	12 SC0308514	AJ308514 Synthetic
34	43.4	68.9	439	6 A41016	A41016 Sequence 3
35	43.4	68.9	439	6 AR082579	AR082579 Sequence
36	43.4	68.9	439	6 I28254	I28254 Sequence 3
37	43.4	68.9	446	6 A78762	A78762 Sequence 23
38	43.4	68.9	446	6 AR014735	AR014735 Sequence
39	43.4	68.9	470	6 AX026717	AX026717 Sequence
40	43.4	68.9	480	12 SYNCAMVCM5	M74305 Synthetic e
41	43.4	68.9	522	6 AX405123	AX405123 Sequence
42	43.4	68.9	532	6 AR110594	AR110594 Sequence
43	43.4	68.9	532	6 AR150993	AR150993 Sequence
44	43.4	68.9	532	6 AR152416	AR152416 Sequence
45	43.4	68.9	532	6 AR152425	AR152425 Sequence

ALIGNMENTS

RESULT 1
AX036610
LOCUS AX036610
DEFINITION Sequence 16 from Patent FR2791358. 63 bp
ACCESSION AX036610
VERSION AX036610.1 GI:11226205
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.
artificial sequences.
REFERENCE
1 (bases 1 to 63)
Rance, I., Theisen, M. and Gruber, V.
Patent: FR 2791358-A 16 29-SEP-2000;
JOURNAL MERISTEM THERAPEUTICS (FR)
FEATURES
Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a

source 1.63
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="directional building block 56-directional building block oligonucleotide for the construction of promoters by 1b-PCR"

BASE COUNT 16 a 14 c 17 g 16 t

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Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 61 ACT 63
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Db 61 ACT 63

RESULT 2
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LOCUS AX036747 63 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 13 from Patent WO0058485.
ACCESSION AX036747
VERSION AX036747.1 GI:11226256
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 63)
AUTHORS Range, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 13 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
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Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="directional desoxyribo-nucleotide building block 56"

BASE COUNT 16 a 14 c 17 g 16 t

Query Match 100.0%; Score 63; DB 6; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CATGCTGCACAGTAGTGATGTGATATCTCCACTGACGTAAAGGATGACGCATGCC 60
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Db 1 CATGCTGCACAGTAGTGATGTGATATCTCCACTGACGTAAAGGATGACGCATGCC 60

OY 61 ACT 63
|||
Db 61 ACT 63

RESULT 3
AX036601
LOCUS AX036601 280 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 7 from Patent FR2791358.
ACCESSION AX036601
VERSION AX036601.1 GI:11226196
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 280)
AUTHORS Range, I., Theisen, M. and Gruber, V.
JOURNAL Patent: FR 2791358-A 7 29-SEP-2000;

FEATURES MERISTEM THERAPEUTICS (FR)
Location/Qualifiers
source 1.280
/organism="synthetic construct"
/db_xref="taxon:32630"

promoter 1.280
/note="The promoter Mp1110 was created by inserting at position -99 bp of Mp1098 an element of 18 bp containing a 'G' box and by fusing a sequence of 44 bp of the RNA 35S CAMV promoter
promoter Mp1110"

BASE COUNT 88 a 73 c 42 g 77 t

Query Match 93.7%; Score 59; DB 6; Length 280;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CTGCAGACTAGTGATGTGATATCTCCACTGACGTAAAGGATGACGCATGCCACT 63
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Db 13 CTGCAGACTAGTGATGTGATATCTCCACTGACGTAAAGGATGACGCATGCCACT 71

RESULT 4
AX036741
LOCUS AX036741 301 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 7 from Patent WO0058485.
ACCESSION AX036741
VERSION AX036741.1 GI:11226250
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 301)
AUTHORS Range, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 7 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES
source 1.301
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter Mp1154"

BASE COUNT 98 a 54 c 74 g 75 t

Query Match 93.7%; Score 59; DB 6; Length 301;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CTGCAGACTAGTGATGTGATATCTCCACTGACGTAAAGGATGACGCATGCCACT 63
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Db 13 CTGCAGACTAGTGATGTGATATCTCCACTGACGTAAAGGATGACGCATGCCACT 71

RESULT 5
AX036740
LOCUS AX036740 398 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 6 from Patent WO0058485.
ACCESSION AX036740
VERSION AX036740.1 GI:11226249
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 398)
AUTHORS Range, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 6 05-OCT-2000;

MERISTEM THERAPEUTICS (FR) ; RANGE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
Location/Qualifiers
1. .398
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/db_xref="taxon:32630"
/note="Promoter MPr1147"
BASE COUNT 128 a 80 c 93 g 97 t
ORIGIN
Promoter 128 a 80 c 93 g 97 t

Query Match 93.7%; Score 59; DB 6; Length 398;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CTGCAGACTAGTGGATTGATGATATCTCCACGTGACGTAAAGGATGACGATGCCACT 63
|||||
Db 110 CTGCAGACTAGTGGATTGATGATATCTCCACGTGACGTAAAGGATGACGATGCCACT 168

RESULT 6
AX036759 472 bp DNA linear PAT 16-NOV-2000
LOCUS AX036759
DEFINITION Sequence 25 from Patent W0058485.
ACCESSION AX036759
VERSION AX036759.1 GI:11226268
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 472)
AUTHORS Range,I., Theisen,M. and Gruber,V.
TITLE Chimeric expression promoters originating from commelina yellow
JOURNAL mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 25 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANGE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
Location/Qualifiers
1. .472
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter MPr1169"
BASE COUNT 149 a 92 c 112 g 119 t
ORIGIN
Promoter 149 a 92 c 112 g 119 t

Query Match 93.7%; Score 59; DB 6; Length 472;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CTGCAGACTAGTGGATTGATGATATCTCCACGTGACGTAAAGGATGACGATGCCACT 63
|||||
Db 110 CTGCAGACTAGTGGATTGATGATATCTCCACGTGACGTAAAGGATGACGATGCCACT 168

RESULT 7
AX036758 541 bp DNA linear PAT 16-NOV-2000
LOCUS AX036758
DEFINITION Sequence 24 from Patent W0058485.
ACCESSION AX036758
VERSION AX036758.1 GI:11226267
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 541)
AUTHORS Range,I., Theisen,M. and Gruber,V.
TITLE Chimeric expression promoters originating from commelina yellow
JOURNAL mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 24 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANGE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
Location/Qualifiers

source 1. .541
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter MPr1168"
BASE COUNT 169 a 104 c 130 g 138 t
ORIGIN
Promoter 169 a 104 c 130 g 138 t

Query Match 93.7%; Score 59; DB 6; Length 541;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CTGCAGACTAGTGGATTGATGATATCTCCACGTGACGTAAAGGATGACGATGCCACT 63
|||||
Db 110 CTGCAGACTAGTGGATTGATGATATCTCCACGTGACGTAAAGGATGACGATGCCACT 168

RESULT 8
AX036757 604 bp DNA linear PAT 16-NOV-2000
LOCUS AX036757
DEFINITION Sequence 23 from Patent W0058485.
ACCESSION AX036757
VERSION AX036757.1 GI:11226266
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 604)
AUTHORS Range,I., Theisen,M. and Gruber,V.
TITLE Chimeric expression promoters originating from commelina yellow
JOURNAL mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 23 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANGE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
Location/Qualifiers
1. .604
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter MPr1167"
BASE COUNT 186 a 116 c 145 g 157 t
ORIGIN
Promoter 186 a 116 c 145 g 157 t

Query Match 93.7%; Score 59; DB 6; Length 604;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CTGCAGACTAGTGGATTGATGATATCTCCACGTGACGTAAAGGATGACGATGCCACT 63
|||||
Db 110 CTGCAGACTAGTGGATTGATGATATCTCCACGTGACGTAAAGGATGACGATGCCACT 168

RESULT 9
AX036611 79 bp DNA linear PAT 16-NOV-2000
LOCUS AX036611
DEFINITION Sequence 17 from Patent FR2791358.
ACCESSION AX036611
VERSION AX036611.1 GI:11226206
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 79)
AUTHORS Range,I., Theisen,M. and Gruber,V.
JOURNAL Patent: FR 2791358-A 17 29-SEP-2000;
MERISTEM THERAPEUTICS (FR)
Location/Qualifiers
1. .79
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="directional building block S7-directional building
block oligonucleotide for the construction of promoters by
1b-PCR"

BASE COUNT 22 a 15 c 20 g 22 t
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Query Match 73.0%; Score 46; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 34 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCACT 79

RESULT 10
LOCUS AX036748 79 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 14 from Patent WO0058485.
ACCESSION AX036748
VERSION AX036748.1 GI:11226257
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 79)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 14 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES
source location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="directional desoxynucleotide building block 87"

BASE COUNT 22 a 15 c 20 g 22 t
ORIGIN

Query Match 73.0%; Score 46; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCACT 63
|||||
DB 34 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCACT 79

RESULT 11
LOCUS AX036616 259 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 22 from Patent FR2791358.
ACCESSION AX036616
VERSION AX036616.1 GI:11226211
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 259)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: FR 2791358-A 22 29-SEP-2000;
MERISTEM THERAPEUTICS (FR)
FEATURES
source location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter Mpri112 differs from Mpri111 by a deletion
of 35 bp containing the 'G' box and stretching from
position -127 to position -89 and a deletion of two bp
situated at positions -78 and -76
promoter Mpri112"

BASE COUNT 82 a 67 c 38 g 72 t
ORIGIN

Query Match 73.0%; Score 46; DB 6; Length 259;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
DB 42 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCACT 87

RESULT 12
LOCUS AX036603 296 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 9 from Patent FR2791358.
ACCESSION AX036603
VERSION AX036603.1 GI:11226198
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 296)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: FR 2791358-A 9 29-SEP-2000;
MERISTEM THERAPEUTICS (FR)
FEATURES
source location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter Mpri111 created by inserting at -99 bp
position of Mpri1098, an 18 bp element containing a 'G' box
and flusing a sequence of 58 bp (duplication of the element
as2 and as1)
promoter Mpri111"

BASE COUNT 94 a 74 c 45 g 83 t
ORIGIN

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Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCACT 63
|||||
DB 42 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCACT 87

RESULT 13
LOCUS AX036739 371 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 5 from Patent WO0058485.
ACCESSION AX036739
VERSION AX036739.1 GI:11226248
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 371)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 5 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
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source location/Qualifiers
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/db_xref="taxon:32630"
/note="promoter Mpri146"

BASE COUNT 122 a 68 c 89 g 92 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.7e-07;

Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 93 GATTGATGTGATATCTCCAGCTAGGATGCGATGCCACT 138

RESULT 14

AX036755/c AX036755 392 bp DNA linear PAT 16-NOV-2000
 DEFINITION Sequence 21 from Patent WO058485.
 ACCESSION AX036755
 VERSION AX036755.1 GI:11226264
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1 (bases 1 to 392)
 AUTHORS Rance,I., Theisen,M. and Gruber,V.
 TITLE ChimERIC expression promoters originating from commelina yellow
 mottle virus and cassava vein mosaic virus
 PATENT: WO 0058485-A 21-05-OCT-2000;
 MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
 ; GRUBER VERONIQUE (FR)

JOURNAL Location/Qualifiers
 source 1..392
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="promoter MPr1164"
 1..392

Promoter 127 a 80 c 87 g 98 t
 BASE COUNT
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 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GATTGATGTGATATCTCCAGCTAGGATGCGATGCCACT 62
 DB 278 GATTGATGTGATATCTCCAGCTAGGATGCGATGCCACT 234

RESULT 15

AX036753 AX036753 393 bp DNA linear PAT 16-NOV-2000
 DEFINITION Sequence 19 from Patent WO058485.
 ACCESSION AX036753
 VERSION AX036753.1 GI:11226262
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1 (bases 1 to 393)
 AUTHORS Rance,I., Theisen,M. and Gruber,V.
 TITLE ChimERIC expression promoters originating from commelina yellow
 mottle virus and cassava vein mosaic virus
 PATENT: WO 0058485-A 19-05-OCT-2000;
 MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
 ; GRUBER VERONIQUE (FR)

JOURNAL Location/Qualifiers
 source 1..393
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="promoter MPr1162"
 1..393

Promoter 128 a 75 c 93 g 97 t
 BASE COUNT
 ORIGIN

Query Match 71.4%; Score 45; DB 6; Length 393;
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 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GATTGATGTGATATCTCCAGCTAGGATGCGATGCCACT 62

DB 258 GATTGATGTGATATCTCCAGCTAGGATGCGATGCCACT 302

Search completed: May 24, 2003, 14:52:24
 Job time : 352.903 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 07:18:51 ; Search time 108.726 Seconds
(without alignments)
1304.896 Million cell updates/sec

Title: US-09-963-803-13

Perfect score: 63
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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	63	21	AAA96847
2	63	100.0	63	21	AAA96471
3	59	93.7	280	21	AAA96463
4	59	93.7	301	21	AAA96841
5	59	93.7	398	21	AAA96840
6	59	93.7	472	21	AAA96859
7	59	93.7	541	21	AAA96858
8	59	93.7	604	21	AAA96857
9	46	73.0	79	21	AAA96848

10	46	73.0	79	21	AAA96472	Nucleotide sequenc
11	46	73.0	259	21	AAA96477	Nucleotide sequenc
12	46	73.0	296	21	AAA96465	Nucleotide sequenc
13	46	73.0	371	21	AAA96839	Nucleotide sequenc
14	45	71.4	392	21	AAA96855	Nucleotide sequenc
15	45	71.4	393	21	AAA96853	Nucleotide sequenc
16	45	71.4	462	21	AAA96854	Nucleotide sequenc
17	45	71.4	600	21	AAA96856	Nucleotide sequenc
18	43.4	68.9	189	22	AAD10066	Amplified product
19	43.4	68.9	240	21	AAAT7895	Soybean RRS gene N
20	43.4	68.9	309	21	AAAT7192	CamV35S promoter e
21	43.4	68.9	309	24	AAD39442	Caulliflower mosaic
22	43.4	68.9	333	22	AAAC83764	Plasmid pMON295 Ca
23	43.4	68.9	334	22	AAAT28369	Nucleotide sequenc
24	43.4	68.9	338	20	AAV99492	Caulliflower mosaic
25	43.4	68.9	350	13	AAQ25533	CamV35S promoter (
26	43.4	68.9	352	13	AAQ25080	CamV 35S promoter,
27	43.4	68.9	395	15	AAQ72688	Caulliflower mosaic
28	43.4	68.9	396	17	AAAT32299	Nucleotide sequenc
29	43.4	68.9	396	22	AAAT28368	Sequence containin
30	43.4	68.9	400	20	AAV99491	35S CMV promoter s
31	43.4	68.9	444	20	AAAT8466	Tomato spotted wil
32	43.4	68.9	444	22	AAAT89658	35S-omega CMV prom
33	43.4	68.9	446	20	AAAT86468	Tomato spotted wil
34	43.4	68.9	446	22	AAAT89660	Chimeric CamV35S-
35	43.4	68.9	470	21	AAA51890	FMV35S90 enhancer
36	43.4	68.9	522	24	AAD39449	Nucleotide sequenc
37	43.4	68.9	532	21	AAAT75458	CamV 35S promoter o
38	43.4	68.9	532	22	AAD06306	Nucleotide sequenc
39	43.4	68.9	532	22	AAD06360	Nucleotide sequenc
40	43.4	68.9	532	22	AAAT89817	Caulliflower mosaic
41	43.4	68.9	532	22	AAAT89826	Caulliflower mosaic
42	43.4	68.9	532	24	AAAT54332	CamV 35S promoter
43	43.4	68.9	550	24	AAD34678	Nucleotide sequenc
44	43.4	68.9	560	21	AAAT75462	CamV 35S promoter o
45	43.4	68.9	560	22	AAD06310	CamV 35S promoter o

ALIGNMENTS

RESULT 1
AAA96847
ID AAA96847 standard; DNA: 63 BP.
AC AAA96847;
XX
XX
XX 19-FEB-2001 (first entry)
XX
XX
XX
XX Directional desoxynucleotide building block S6.
XX
XX Promoter; intergenic region; Comelina yellow mottle virus;
XX chimeric expression promoter; plant vascular expression promoter;
XX plant green tissue expression promoter; Cassava vein mosaic virus;
XX transgenic plant; ss.
XX
XX
XX Synthetic.
XX
XX WO200058485-A1.
XX
XX 05-OCT-2000.
XX
XX 29-MAR-2000; 2000WO-1B00370.
XX
XX
XX 29-MAR-1999; 99FR-0003925.
XX
XX
XX (MERI-) MERISTEM THERAPEUTICS.
XX
XX Rance I, Gruber V, Theisen M;
XX
XX WPI: 2000-647238/62.
XX
XX
XX Chimeric expression promoter for transgenic plant production, comprises

PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX
XX Disclosure: Page 30; 91pp; English.
XX
XX The present sequence represents a directional desoxynucleotide building
CC block, which was used to construct chimeric promoters of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Comellina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
XX Sequence 63 BP; 16 A; 14 C; 17 G; 16 T; 0 other;
SQ
Query Match 100.0%; Score 63; DB 21; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATGCTGCACAGTACGATGATGATGATATCTCCACTGACGTAAGGATGACGCATGCC 60
DB 1 CATGCTGCACAGTACGATGATGATGATATCTCCACTGACGTAAGGATGACGCATGCC 60
QY 61 ACT 63
DB 61 ACT 63
RESULT 2
AAA96471
ID AAA96471 standard; DNA; 63 BP.
XX
XX AAA96471;
AC
XX
XX 08-FEB-2001 (first entry)
DT
XX
XX Nucleotide sequence of the directional building block S6.
DE
XX
XX pete promoter; chimeric promoter; transgenic plant; MPr1108;
KW plastocyanin gene promoter; PCR primer; ss.
XX
XX Synthetic.
OS
XX
XX WO200056906-A1.
PN
XX
XX 28-SEP-2000.
PD
XX
XX 20-MAR-2000; 2000WO-IB00317.
PF
XX
XX 22-MAR-1999; 99FR-0003635.
PR
XX
XX (MERI-) MERISTEM THERAPEUTICS.
PA
XX
XX Rance I, Gruber V, Theisen M;
PI
XX
XX WPI; 2000-587667/55.
DR
XX
XX Chimeric expression promoter for producing dicotyledonous and
PT monocotyledonous transgenic plants comprises a nucleic acid sequence
PT derived from a promoter of the pea plastocyanin gene -
XX
XX Claim 24; Page 75; 83pp; English.
PS
XX
XX The present sequence represents the directional building block S6,
CC which is used to construct chimeric promoters of the invention in
CC PCR reactions. The specification describes a chimeric expression
CC promoter comprising a pete promoter of the pea plastocyanin gene, or

CC comprising a G box operably or functionally linked upstream of a
CC CAAT box, TATA box and transcription initiation site. The chimeric
CC promoters are used in expression vectors for producing transgenic
CC plants, such as dicotyledonous species, e.g. potato, tobacco, cotton,
CC lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower,
CC and monocotyledonous species, e.g. wheat, barley, oat, rice, or corn.
XX
XX Sequence 63 BP; 16 A; 14 C; 17 G; 16 T; 0 other;
SQ
Query Match 100.0%; Score 63; DB 21; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATGCTGCACAGTACGATGATGATGATATCTCCACTGACGTAAGGATGACGCATGCC 60
DB 1 CATGCTGCACAGTACGATGATGATGATATCTCCACTGACGTAAGGATGACGCATGCC 60
QY 61 ACT 63
DB 61 ACT 63
RESULT 3
AAA96463
ID AAA96463 standard; DNA; 280 BP.
XX
XX AAA96463;
AC
XX
XX 08-FEB-2001 (first entry)
DT
XX
XX Nucleotide sequence of the promoter MPr1110.
DE
XX
XX pete promoter; chimeric promoter; transgenic plant; MPr1110;
KW plastocyanin gene promoter; ss.
XX
XX Synthetic.
OS
XX
XX Plasm sativum.
PN
XX
XX WO200056906-A1.
PD
XX
XX 28-SEP-2000.
PF
XX
XX 20-MAR-2000; 2000WO-IB00317.
PR
XX
XX 22-MAR-1999; 99FR-0003635.
PA
XX
XX (MERI-) MERISTEM THERAPEUTICS.
PI
XX
XX Rance I, Gruber V, Theisen M;
PI
XX
XX WPI; 2000-587667/55.
DR
XX
XX Chimeric expression promoter for producing dicotyledonous and
PT monocotyledonous transgenic plants comprises a nucleic acid sequence
PT derived from a promoter of the pea plastocyanin gene -
XX
XX Claim 2; Page 70; 83pp; English.
PS
XX
XX The present sequence represents the chimeric promoter MPr1110. The
CC promoter is derived from the pete promoter from pea plastocyanin gene,
CC by fusing the pete as-1 like and nos enhancer like elements to the
CC promoter MPr1098 (comprising TATA and CAAT boxes of pete) and then
CC inserting a G box and fusing a Fragment of 35S RNA of CMV. The pete
CC promoter directs cell-specific but not full light-regulated expression in
CC transgenic tobacco plants. The promoter is used to construct chimeric
CC promoters of the invention. The specification describes a chimeric
CC expression promoter comprising a promoter of the pea plastocyanin gene,
CC or comprising a G box operably or functionally linked upstream of a CAAT
CC box, TATA box and transcription initiation site. The chimeric promoters
CC are used in expression vectors for producing transgenic plants, such as
CC dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato,
CC melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous
CC species, e.g. wheat, barley, oat, rice, or corn.

KM Promoter: intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
PN WO200058485-A1.
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000MO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI; 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
PS Claim 5; Page 88; 91pp; English.
XX
CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 472 BP; 149 A; 92 C; 112 G; 119 T; 0 other;
XX
Query Match 93.7%; Score 59; DB 21; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 5 CTCGACACTAGTGGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCACT 63
DB 110 CTGCAGACTAGTGGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCACT 168
XX
RESULT 7
AAA96858
ID AAA96858 standard; DNA: 541 BP.
XX
AC AAA96858;
XX
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter MPr1168.
XX
KM Promoter: intergenic region; Commelina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
PN WO200058485-A1.
PD 05-OCT-2000.

XX
PF 29-MAR-2000; 2000MO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI; 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
PS Claim 5; Page 87-88; 91pp; English.
XX
CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 541 BP; 169 A; 104 C; 130 G; 138 T; 0 other;
XX
Query Match 93.7%; Score 59; DB 21; Length 541;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 5 CTCGACACTAGTGGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCACT 63
DB 110 CTGCAGACTAGTGGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCACT 168
XX
RESULT 8
AAA96857
ID AAA96857 standard; DNA: 604 BP.
XX
AC AAA96857;
XX
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter MPr1167.
XX
KM Promoter: intergenic region; Commelina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
PN WO200058485-A1.
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000MO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI; 2000-647238/62.
XX

PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
PS Claim 5; Page 87; 91pp: English.
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 604 BP; 186 A; 116 C; 145 G; 157 T; 0 other;
Query Match 93.7%; Score 59; DB 21; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 CTGCAGACTAGTGGATTGATGTCATCTCCACTGACGTAGGAGTACGCATGCCACT 63
DB 110 CTGCAGACTAGTGGATTGATGTCATCTCCACTGACGTAGGAGTACGCATGCCACT 168
RESULT 9
AAA96848
ID AAA96848 standard; DNA; 79 BP.
XX
AC AAA96848;
XX
DT 19-FEB-2001 (first entry)
XX
DE Directional desoxynucleotide building block S7.
XX
XX Promoter; intergenic region; Commelina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; ss.
XX
OS Synthetic.
XX
PN WO200058485-A1.
XX
XX 05-OCT-2000.
XX
XX 29-MAR-2000; 2000WO-IB00370.
XX
XX 29-MAR-1999; 99FR-0003925.
XX
XX (MERI-) MERISTEM THERAPEUTICS.
XX
XX Rance I, Gruber V, Theisen M;
XX
XX WPI; 2000-647238/62.
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX Disclosure; Page 26; 91pp: English.
XX
XX The present sequence represents a directional desoxynucleotide building
CC block, which was used to construct chimeric promoters of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression

CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 79 BP; 22 A; 15 C; 20 G; 22 T; 0 other;
Query Match 73.0%; Score 46; DB 21; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 18 GATTGATGTGATATCTCCACTGACGTAGGAGTACGCATGCCACT 63
DB 34 GATTGATGTGATATCTCCACTGACGTAGGAGTACGCATGCCACT 79
RESULT 10
AAA96472
ID AAA96472 standard; DNA; 79 BP.
XX
XX AAA96472;
XX
AC 08-FEB-2001 (first entry)
XX
DT Nucleotide sequence of the directional building block S7.
XX
DE
XX
XX pete promoter; chimeric promoter; transgenic plant; Mpr1108;
KM plastocyanin gene promoter; PCR primer; ss.
KM
XX Synthetic.
XX
XX WO200056906-A1.
XX
XX 28-SEP-2000.
XX
XX 20-MAR-2000; 2000WO-IB00317.
XX
XX 22-MAR-1999; 99FR-0003635.
XX
XX (MERI-) MERISTEM THERAPEUTICS.
XX
XX Rance I, Gruber V, Theisen M;
XX
XX WPI; 2000-587667/55.
XX
XX Chimeric expression promoter for producing dicotyledonous and
PT monocotyledonous transgenic plants comprises a nucleic acid sequence
PT derived from a promoter of the pea plastocyanin gene
PT
XX
XX Claim 24; Page 76; 83pp: English.
XX
XX The present sequence represents the directional building block S7,
CC which is used to construct chimeric promoters of the invention in
CC PCR reactions. The specification describes a chimeric expression
CC promoter comprising a pete promoter of the pea plastocyanin gene, or
CC comprising a G box operably or functionally linked upstream of a
CC CAAT box, TATA box and transcription initiation site. The chimeric
CC promoters are used in expression vectors for producing transgenic
CC plants, such as dicotyledonous species, e.g. potato, tobacco, cotton,
CC lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower,
CC and monocotyledonous species, e.g. wheat, barley, oat, rice, or corn.
XX
SQ Sequence 79 BP; 22 A; 15 C; 20 G; 22 T; 0 other;
Query Match 73.0%; Score 46; DB 21; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 18 GATTGATGTGATATCTCCACTGACGTAGGAGTACGCATGCCACT 63
DB 34 GATTGATGTGATATCTCCACTGACGTAGGAGTACGCATGCCACT 79

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DB 34 GATTGATGTGATATCTCCACTGACGTAAAGGATGAGCATGGCACT 79

RESULT 11
ID AAA96477 standard; DNA; 259 BP.
XX AAA96477;
AC
XX
XX
XX 08-FEB-2001 (first entry)
XX
XX Nucleotide sequence of the promoter Mp1112.
XX
XX petE promoter; chimeric promoter; transgenic plant; Mp1112;
XX plastocyanin gene promoter; ss.
XX
XX Pisum sativum.
XX
XX WO200056906-A1.
XX
XX 28-SEP-2000.
XX
XX 20-MAR-2000; 2000WO-1B00317.
XX
XX 22-MAR-1999; 99FR-0003635.
XX
XX (MERI-) MERISTEM THERAPEUTICS.
XX
XX Rance I, Gruber V, Thelsen M;
XX
XX MPI: 2000-587667/55.
XX
XX Chimeric expression promoter for producing dicotyledonous and
XX monocotyledonous transgenic plants comprises a nucleic acid sequence
XX derived from a promoter of the pea plastocyanin gene
XX
XX Claim 25; Page 79; 83pp; English.
XX
XX The present sequence represents the chimeric promoter Mp1112. The
XX promoter is derived from the petE promoter from pea plastocyanin gene,
XX by fusing the petE as-1 like and nos enhancer like elements to the
XX promoter Mp1098 (comprising TATA and CAAT boxes of petE), and then
XX fusing a fragment comprising a duplication of the element as2 and as1.
XX The petE promoter directs cell-specific but not full light-regulated
XX expression in transgenic tobacco plants. The promoter is used to
XX construct chimeric promoters of the invention. The specification
XX describes a chimeric expression promoter comprising a promoter of
XX the pea plastocyanin gene, or comprising a G box operably or
XX functionally linked upstream of a CAAT box, TATA box and transcription
XX initiation site. The chimeric promoters are used in expression vectors
XX for producing transgenic plants, such as dicotyledonous species,
XX e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea,
XX rapa, beetroot, or sunflower, and monocotyledonous species, e.g. wheat,
XX barley, oat, rice, or corn.
XX
XX Sequence 259 BP; 82 A; 67 C; 38 G; 72 T; 0 other;
XX
XX Query Match 73.0%; Score 45; DB 21; Length 259;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-06;
XX Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX 18 GATTGATGTGATATCTCCACTGACGTAAAGGATGAGCATGGCACT 63
XX |||||
XX 42 GATTGATGTGATATCTCCACTGACGTAAAGGATGAGCATGGCACT 87
XX
XX RESULT 12
XX ID AAA96465 standard; DNA; 296 BP.
XX
XX AAA96465;
XX
XX
XX
XX 08-FEB-2001 (first entry)
XX

```

XX	Nucleotide sequence of the promoter MpRII1.
DE	
XX	pete promoter; chimeric promoter; transgenic plant; MpRII1;
KW	plastocyanin gene promoter; ss.
XX	Synthetic.
OS	Plasm sativum.
XX	wO200056906-A1.
PN	
PD	28-SEP-2000.
PF	20-MAR-2000; 2000WO-IB00317.
XX	
PR	22-MAR-1999; 99FR-0003635.
PA	(MER-) MERISTEM THERAPEUTICS.
XX	
PI	Rance I, Gruber V, Thelsen M;
XX	
DR	WPI: 2000-587667/55.
PT	Chimeric expression promoter [*] for producing dicotyledonous and monocotyledonous transgenic plants comprises a nucleic acid sequence derived from a promoter of the pea plastocyanin gene
PS	Claim 2; Page 71; 83pp; English.
XX	The present sequence represents the chimeric promoter MpriII1. The promoter is derived from the pete promoter from pea plastocyanin gene, by fusing the pete as-1 like and nos enhancer like elements to the promoter MPRI098 (comprising TAFA and CAAT boxes of pete), and then inserting a G box and fusing a fragment comprising a duplication of the element aa2 and asl. The pete promoter directs cell-specific but not full light-regulated expression in transgenic tobacco plants. The promoter is used to construct chimeric promoters of the invention. The specification describes a chimeric expression promoter comprising a promoter of the pea plastocyanin gene, or comprising a G box operably or functionally linked upstream of a CAAT box, TAFA box and transcription initiation site. The chimeric promoters are used in expression vectors for producing transgenic plants, such as dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat, barley, oat, rice, or corn.
CC	
CO	Sequence 296 BP; 94 A; 74 C; 45 G; 83 T; 0 other;
SO	
Query Match	73.0%; Score 46; DB 21; Length 296;
Best Local Similarity	100.0%; Pred. No. 2e-08;
Matches	46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	18 GATTGATGTGATATCTCCACGTAGCGTAAAGGATGACGCATGCCACT 63 42 GATTGATGTGATATCTCCACGTAGCGTAAAGGATGACGCATGCCACT 87
DJ	
RESULT 13	
ID	AAA96839 standard; DNA; 371 BP.
AAA96839	
AC	AAA96839;
DT	19-FEB-2001 (first entry)
DE	
XX	Nucleotide sequence of chimeric expression promoter MpRII46.
XX	
XX	Promoter; intergenic region; Commelina yellow mottle virus; chimeric expression promoter; plant vascular expression promoter; plant green tissue expression promoter; Cassava vein mosaic virus; transgenic plant; chimera; ss.
KW	
XX	Chimeric - Commelina yellow mottle virus.
DS	

OS Chimeric - Cassava vein mosaic virus.
 XX
 PN WO200058485-A1.
 XX
 PD 05-OCT-2000.
 XX
 XX 29-MAR-2000; 2000WO-IB00370.
 PF
 XX 29-MAR-1999; 99FR-0003925.
 PR
 XX
 PA (MERIT-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theisen M;
 XX
 DR WPI; 2000-647238/62.
 XX
 PT Chimeric expression promoter for transgenic plant production, comprises
 PT sequence from promoter comprising vascular expression region replaced
 PT with sequence from promoter comprising green tissue expression region
 PT
 XX
 PS Claim 5; Page 81; 91pp; English.
 CC The present sequence represents a chimeric promoter of the invention.
 CC The specification describes chimeric expression promoters. These
 CC chimeric promoters comprise a nucleic acid sequence which is derived
 CC from a first plant promoter, in which a plant vascular expression
 CC promoter region is replaced with a nucleic acid sequence derived from
 CC a second plant promoter comprising a plant green tissue expression
 CC promoter region. Preferably, the first plant promoter originates from
 CC Commelina yellow mottle virus, and the second plant promoter originates
 CC from the Cassava vein mosaic virus. Especially, the promoters are
 CC derived from intergenic regions. The chimeric promoters are useful
 CC for producing transgenic plants.
 XX
 SQ Sequence 371 BP; 122 A; 68 C; 89 G; 92 T; 0 other:
 Query Match 73.0%; Score 46; DB 21; Length 371;
 Best Local Similarity 100.0%; Pred. No. 2.1e-08;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 GATTGATGTGATATCTCCACGTAGGATGAGGATGCCACT 63
 DB 93 GATTGATGTGATATCTCCACGTAGGATGAGGATGCCACT 138
 RESULT 14
 AAA96855/c
 ID AAA96855 standard; DNA; 392 BP.
 AC
 XX AAA96855;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 DE Nucleotide sequence of chimeric expression promoter MPr1164.
 XX
 KW Promoter; intergenic region; Commelina yellow mottle virus;
 KW chimeric expression promoter; plant vascular expression promoter;
 KW plant green tissue expression promoter; Cassava vein mosaic virus;
 KW transgenic plant; chimera; ss.
 XX
 OS Chimeric - Commelina yellow mottle virus.
 OS Chimeric - Cassava vein mosaic virus.
 XX
 PN WO200058485-A1.
 XX
 PD 05-OCT-2000.
 XX
 XX 29-MAR-2000; 2000WO-IB00370.
 PF
 XX 29-MAR-1999; 99FR-0003925.
 PR
 XX
 PA (MERIT-) MERISTEM THERAPEUTICS.

XX
 PI Rance I, Gruber V, Theisen M;
 XX
 DR WPI; 2000-647238/62.
 XX
 XX Chimeric expression promoter for transgenic plant production, comprises
 PT sequence from promoter comprising vascular expression region replaced
 PT with sequence from promoter comprising green tissue expression region
 PT
 XX
 PS Claim 5; Page 86; 91pp; English.
 CC The present sequence represents a chimeric promoter of the invention.
 CC The specification describes chimeric expression promoters. These
 CC chimeric promoters comprise a nucleic acid sequence which is derived
 CC from a first plant promoter, in which a plant vascular expression
 CC promoter region is replaced with a nucleic acid sequence derived from
 CC a second plant promoter comprising a plant green tissue expression
 CC promoter region. Preferably, the first plant promoter originates from
 CC Commelina yellow mottle virus, and the second plant promoter originates
 CC from the Cassava vein mosaic virus. Especially, the promoters are
 CC derived from intergenic regions. The chimeric promoters are useful
 CC for producing transgenic plants.
 CC
 SQ Sequence 392 BP; 127 A; 80 C; 87 G; 98 T; 0 other:
 Query Match 71.4%; Score 45; DB 21; Length 392;
 Best Local Similarity 100.0%; Pred. No. 5.3e-08;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 GATTGATGTGATATCTCCACGTAGGATGAGGATGCCACT 62
 DB 278 GATTGATGTGATATCTCCACGTAGGATGAGGATGCCACT 234
 RESULT 15
 AAA96853
 ID AAA96853 standard; DNA; 393 BP.
 AC
 XX AAA96853;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 DE Nucleotide sequence of chimeric expression promoter MPr1162.
 XX
 KW Promoter; intergenic region; Commelina yellow mottle virus;
 KW chimeric expression promoter; plant vascular expression promoter;
 KW plant green tissue expression promoter; Cassava vein mosaic virus;
 KW transgenic plant; chimera; ss.
 XX
 OS Chimeric - Commelina yellow mottle virus.
 OS Chimeric - Cassava vein mosaic virus.
 XX
 PN WO200058485-A1.
 XX
 PD 05-OCT-2000.
 XX
 XX 29-MAR-2000; 2000WO-IB00370.
 PF
 XX 29-MAR-1999; 99FR-0003925.
 PR
 XX
 PA (MERIT-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theisen M;
 XX
 DR WPI; 2000-647238/62.
 XX
 PT Chimeric expression promoter for transgenic plant production, comprises
 PT sequence from promoter comprising vascular expression region replaced
 PT with sequence from promoter comprising green tissue expression region
 PT
 XX
 PS Claim 5; Page 85; 91pp; English.

XX The present sequence represents a chimeric promoter of the invention.
 CC The specification describes chimeric expression promoters. These
 CC chimeric promoters comprise a nucleic acid sequence which is derived
 CC from a first plant promoter, in which a plant vascular expression
 CC promoter region is replaced with a nucleic acid sequence derived from
 CC a second plant promoter comprising a plant green tissue expression
 CC promoter region. Preferably, the first plant promoter originates from
 CC *Commelina* yellow mottle virus, and the second plant promoter originates
 CC from the *Cassava* vein mosaic virus. Especially, the promoters are
 CC derived from intergenic regions. The chimeric promoters are useful
 CC for producing transgenic plants.
 XX
 XX Sequence 393 BP; 128 A; 75 C; 93 G; 97 T; 0 other;
 50
 Query Match 71.4%; Score 45; DB 21; Length 393;
 Best Local Similarity 100.0%; Pred. No. 5.3e-08;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 0y 18 GATTGATGTGATATCTCCACCTGACCTAAGGATGACGCATGCCAC 62
 |||||||
 Db 258 GATTGATGTGATATCTCCACCTGACCTAAGGATGACGCATGCCAC 302

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Search completed: May 24, 2003, 14:34:44
Job time : 109.726 secs
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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 13:52:01 ; Search time 26.0806 Seconds
(Without alignments)
740.804 Million cell updates/sec

Title: US-09-963-803-13

Perfect score: 63
Sequence: 1 catgctgcagactagtgat.....aaggatgacatgacct 63

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
1	43.4	68.9	439	1	US-08-247-809A-3	Sequence 3, Appli
2	43.4	68.9	439	2	US-08-711-728-3	Sequence 3, Appli
3	43.4	68.9	446	1	US-08-764-100-23	Sequence 23, Appli
4	43.4	68.9	532	3	US-09-042-426-1	Sequence 1, Appli
5	43.4	68.9	532	4	US-09-291-238-1	Sequence 1, Appli
6	43.4	68.9	532	4	US-09-330-760-1	Sequence 1, Appli
7	43.4	68.9	532	4	US-09-328-473-1	Sequence 1, Appli
8	43.4	68.9	532	4	US-09-330-737-1	Sequence 1, Appli
9	43.4	68.9	532	4	US-09-329-169-1	Sequence 1, Appli
10	43.4	68.9	532	4	US-09-330-714A-1	Sequence 1, Appli
11	43.4	68.9	532	4	US-09-328-826-1	Sequence 1, Appli
12	43.4	68.9	560	3	US-09-042-426-5	Sequence 5, Appli
13	43.4	68.9	560	4	US-09-291-238-5	Sequence 5, Appli
14	43.4	68.9	560	4	US-09-330-760-5	Sequence 5, Appli
15	43.4	68.9	560	4	US-09-328-473-5	Sequence 5, Appli
16	43.4	68.9	560	4	US-09-330-737-5	Sequence 5, Appli
17	43.4	68.9	560	4	US-09-329-169-5	Sequence 5, Appli
18	43.4	68.9	560	4	US-09-330-714A-5	Sequence 5, Appli
19	43.4	68.9	560	4	US-09-328-826-5	Sequence 5, Appli
20	43.4	68.9	661	4	US-09-027-998A-33	Sequence 33, Appli
21	43.4	68.9	793	1	US-08-371-764-1	Sequence 1, Appli
22	43.4	68.9	793	1	US-08-897-736-1	Sequence 1, Appli
23	43.4	68.9	831	1	US-08-450-834-5	Sequence 5, Appli
24	43.4	68.9	950	6	5177308-3	Patent No. 5177308
25	43.4	68.9	978	1	US-08-446-486-31	Sequence 31, Appli
26	43.4	68.9	978	1	US-08-463-308-31	Sequence 31, Appli
27	43.4	68.9	979	1	US-08-446-486-30	Sequence 30, Appli

28	43.4	68.9	979	1	US-08-463-308-30	Sequence 30, Appli
29	43.4	68.9	980	6	5254799-30	Patent No. 5254799
30	43.4	68.9	1030	1	US-07-936-163-46	Sequence 46, Appli
31	43.4	68.9	1030	4	US-08-728-601A-43	Sequence 43, Appli
32	43.4	68.9	1034	4	US-09-363-970-35	Sequence 35, Appli
33	43.4	68.9	1138	4	US-09-011-151-8	Sequence 8, Appli
34	43.4	68.9	1138	4	US-09-011-151-9	Sequence 9, Appli
35	43.4	68.9	1196	4	US-08-729-601A-46	Sequence 46, Appli
36	43.4	68.9	1279	4	US-09-185-244-2	Sequence 2, Appli
37	43.4	68.9	1279	4	US-09-471-913-6	Sequence 6, Appli
38	43.4	68.9	1303	3	US-08-894-440-2	Sequence 2, Appli
39	43.4	68.9	1303	4	US-09-458-093-2	Sequence 2, Appli
40	43.4	68.9	1651	3	US-09-065-999-5	Sequence 5, Appli
41	43.4	68.9	1651	3	US-09-065-999-6	Sequence 6, Appli
42	43.4	68.9	1722	1	US-08-247-809A-5	Sequence 5, Appli
43	43.4	68.9	1722	2	US-08-711-728-5	Sequence 5, Appli
44	43.4	68.9	1829	1	US-07-966-167-17	Sequence 17, Appli
45	43.4	68.9	1863	1	US-08-525-507-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1
US-08-247-809A-3
Sequence 3, Application US/08247809A
Patent No. 5569823

GENERAL INFORMATION:

APPLICANT: Peter H. Schreier; Klaus Stenzel; Gunter Adam;

APPLICANT: Edgar Maiss

TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: SPRUNG HORN KRAMER & WOODS

STREET: 660 White Plains Road

CITY: Tarrytown

STATE: New York

COUNTRY: U.S.A.

ZIP: 10591-5144

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB

COMPUTER: NEC Powermate 1 Plus

OPERATING SYSTEM: DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/247,809A

FILING DATE: May 23, 1994

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: P 43 178 45.6 (Germany)

FILING DATE: May 28, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Kurt G. Briscoe

REGISTRATION NUMBER: 33,141

REFERENCE/DOCKET NUMBER: Bayer 9049-RGB

TELECOMMUNICATION INFORMATION:

TELEPHONE: (914) 332-1700

TELEFAX: (914) 332-1844

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 439 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-247-809A-3

Query Match 68.9% Score 43.4; DB 1; Length 439;
Best Local Similarity 97.8%; Pred. No. 4, 3e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CTAGTGATGATGATGATATCTCCACTGACGTAAAGGATGACGCA 56
DB 332 CAAGTGATGATGATGATATCTCCACTGACGTAAAGGATGACGCA 376

RESULT 2

US-08-711-728-3
Sequence 3, Application US/08711728
Patent No. 5973135
GENERAL INFORMATION:
APPLICANT: Peter H. Schreier; Klaus Stenzel; Gunter Adam;
APPLICANT: Edgar Maiss
TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPRUNG HORN KRAMER & WOODS
STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
OPERATING SYSTEM: DOS
COMPUTER: NEC Powermate 1 Plus
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/711,728
FILING DATE: 03-SEPT-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/247,809
FILING DATE: 23-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 43178456
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 9049.1-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 439 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-711-728-3

Query Match 68.9%; Score 43.4; DB 2; Length 439;
Best Local Similarity 97.8%; Pred. No. 4.3e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CTAGTGATGATGATGATATCTCCACTGACGTAAAGGATGACGCA 56
DB 332 CAAGTGATGATGATGATATCTCCACTGACGTAAAGGATGACGCA 376

RESULT 3
US-08-764-100-23
Sequence 23, Application US/08764100
Patent No. 5773700
GENERAL INFORMATION:
APPLICANT: Van Grinsven J., Martinus O.
APPLICANT: De Haan, Petrus T.
APPLICANT: Giesen L., Johannes J.
APPLICANT: Peters, Dirk
APPLICANT: Goldbach, Robert W.

TITLE OF INVENTION: Improvements in or Relating to Organic
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sandoz Agro, Inc
STREET: 975 California Avenue
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,100
FILING DATE: 06-DEC-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,064
FILING DATE:
APPLICATION NUMBER: US 08/032,235
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: GB 9206016.9
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 57737001s, Allen E.
REGISTRATION NUMBER: 34,490
REFERENCE/DOCKET NUMBER: 137-1061
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 354-3592
TELEFAX: (415) 857-1125
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-764-100-23

Query Match 68.9%; Score 43.4; DB 1; Length 446;
Best Local Similarity 97.8%; Pred. No. 4.3e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CTAGTGATGATGATGATATCTCCACTGACGTAAAGGATGACGCA 56
DB 268 CAAGTGATGATGATGATATCTCCACTGACGTAAAGGATGACGCA 312

RESULT 4

US-09-042-426-1
Sequence 1, Application US/09042426
Patent No. 6114608
GENERAL INFORMATION:
APPLICANT: Irvan J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6114608artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: March 13, 1998

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-042-426-1

Query Match 68.9%; Score 43.4; DB 3; Length 532;
Best Local Similarity 97.8%; Pred. No. 4.6e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 CTAGTGATGTGATGATATCTCCACGTGAGGATGACGCA 56
|
Db 268 CAAGTGATGTGATGATATCTCCACGTGAGGATGACGCA 312

RESULT 5
US-09-291-238-1
Sequence 1, Application US/09291238
Patent No. 6222104

GENERAL INFORMATION:
APPLICANT: Irvlin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 6222104artls Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,238
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO

IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-291-238-1

Query Match 68.9%; Score 43.4; DB 4; Length 532;
Best Local Similarity 97.8%; Pred. No. 4.6e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 CTAGTGATGTGATGATATCTCCACGTGAGGATGACGCA 56
|
Db 268 CAAGTGATGTGATGATATCTCCACGTGAGGATGACGCA 312

RESULT 6
US-09-330-760-1
Sequence 1, Application US/09330760
Patent No. 6229075

GENERAL INFORMATION:
APPLICANT: Irvlin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 6229075artls Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,760
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-330-760-1

Query Match 68.9%; Score 43.4; DB 4; Length 532;
Best Local Similarity 97.8%; Pred. No. 4.6e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 CTAGTGATGTGATGATATCTCCACGTGAGGATGACGCA 56
|
Db 268 CAAGTGATGTGATGATATCTCCACGTGAGGATGACGCA 312

RESULT 7
US-09-328-473-1
Sequence 1, Application US/09328473
Patent No. 6232533

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APPLICATION NUMBER: US/09/330.737
MATCHES:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/042.426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-330-737-1

Query Match          68.9%; Score 43.4; DB 4; Length 532;
Best Local Similarity 97.8%; Pred. No. 4,6e-09;
Matches   44; Conservative    0; Mismatches     1; Indels      0; Gaps       0

OY      12 CTAGTGATTTGATGTGATATCTCCACTGCAGTAAGGATGACCGCA 56
         | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      268 CAAGTGGATTTGATGTGATATCTCCACTGCAGTAAGGATGACCGCA 312

RESULT 9
US-09-329-169-1
Sequence 1, Application US/09329169
Patent No. 6329575
GENERAL INFORMATION:
APPLICANT: Irvlin J. Mettler, Paul S. Dietrich, Ralph Stinabaldt
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6329575artls Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,169
FILING DATE: 09-Jun-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid

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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-329-169-1

Query Match 68.9%; Score 43.4; DB 4; Length 532;
Best Local Similarity 97.8%; Pred. No. 4.6e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

12 CTAAGTGGATTGATGATATCTCCACTGACGTAAAGGATGACGCA 56
DB 268 CAAGTGGATTGATGATATCTCCACTGACGTAAAGGATGACGCA 312

RESULT 10
US-09-330-714A-1
Sequence 1, Application US/09330714A
Patent No. 6342660
GENERAL INFORMATION:
APPLICANT: Irvin J. Wettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
Thuringiensis Gene
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6342660artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,714A
FILING DATE: 11-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-330-714A-1

Query Match 68.9%; Score 43.4; DB 4; Length 532;
Best Local Similarity 97.8%; Pred. No. 4.6e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

12 CTAAGTGGATTGATGATATCTCCACTGACGTAAAGGATGACGCA 56

DB 268 CAAGTGGATTGATGATATCTCCACTGACGTAAAGGATGACGCA 312

RESULT 11
US-09-328-826-1
Sequence 1, Application US/09328826
Patent No. 639860
GENERAL INFORMATION:
APPLICANT: Irvin J. Wettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 639860artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/328,826
FILING DATE: 09-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-328-826-1

Query Match 68.9%; Score 43.4; DB 4; Length 532;
Best Local Similarity 97.8%; Pred. No. 4.6e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

12 CTAAGTGGATTGATGATATCTCCACTGACGTAAAGGATGACGCA 56
DB 268 CAAGTGGATTGATGATATCTCCACTGACGTAAAGGATGACGCA 312

RESULT 12
US-09-042-426-5
Sequence 5, Application US/09042426
Patent No. 6114608
GENERAL INFORMATION:
APPLICANT: Irvin J. Wettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 611460artis Corporation
STREET: 564 Morris Avenue
CITY: Summit

STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: March 13, 1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-042-426-5

Query Match 68.9%; Score 43.4; DB 3; Length 560;
Best Local Similarity 97.8%; Pred. No. 4.7e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 CTAAGTGGATTGATGATATCTCCACTGACGTAAGGATGACGCA 56
DB 316 CAAGTGGATTGATGATATCTCCACTGACGTAAGGATGACGCA 360

RESULT 13
US-09-291-238-5
Sequence 5, Application US/09291238
Patent No. 6222104
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6222104artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,238
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-291-238-5

Query Match 68.9%; Score 43.4; DB 4; Length 560;
Best Local Similarity 97.8%; Pred. No. 4.7e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 CTAAGTGGATTGATGATATCTCCACTGACGTAAGGATGACGCA 56
DB 316 CAAGTGGATTGATGATATCTCCACTGACGTAAGGATGACGCA 360

RESULT 14
US-09-330-760-5
Sequence 5, Application US/09330760
Patent No. 6229075
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6229075artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,760
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-330-760-5

Query Match 68.9%; Score 43.4; DB 4; Length 560;
Best Local Similarity 97.8%; Pred. No. 4.7e-09;

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 13:48:31 ; Search time 49,1129 Seconds
(without alignments)
1693.834 Million cell updates/sec

Title: US-09-963-803-13

Perfect score: 63

Sequence: 1 catctgcagactagatgagat.....aaggatgacgacgacact 63

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 66021138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	100.0	63	US-09-963-803-13	Sequence 13, Appl
2	59	93.7	301	US-09-963-803-7	Sequence 7, Appl
3	59	93.7	398	US-09-963-803-6	Sequence 21, Appl
4	59	93.7	472	US-09-963-803-25	Sequence 25, Appl
5	59	93.7	541	US-09-963-803-24	Sequence 24, Appl
6	59	93.7	604	US-09-963-803-23	Sequence 22, Appl
7	46	73.0	79	US-09-963-803-14	Sequence 14, Appl
8	46	73.0	371	US-09-963-803-5	Sequence 5, Appl
9	45	71.4	392	US-09-963-803-21	Sequence 21, Appl
10	45	71.4	393	US-09-963-803-19	Sequence 19, Appl
11	45	71.4	462	US-09-963-803-20	Sequence 20, Appl
12	45	71.4	600	US-09-963-803-22	Sequence 22, Appl
13	43.4	68.9	309	US-10-012-070A-47	Sequence 47, Appl
14	43.4	68.9	566	US-09-951-470-3	Sequence 3, Appl
15	43.4	68.9	661	US-09-943-692-33	Sequence 33, Appl
16	43.4	68.9	700	US-10-138-221-9	Sequence 9, Appl
17	43.4	68.9	763	US-10-162-214-9	Sequence 9, Appl
18	43.4	68.9	829	US-10-109-812-10	Sequence 10, Appl
19	43.4	68.9	3983	US-09-758-987-1	Sequence 1, Appl

20	43.4	68.9	4973	US-09-990-659A-15	Sequence 15, Appl
21	43.4	68.9	5767	US-09-810-861B-3	Sequence 3, Appl
22	43.4	68.9	6426	US-09-316-622-3	Sequence 3, Appl
23	43.4	68.9	6500	US-09-316-622-4	Sequence 4, Appl
24	43.4	68.9	6750	US-09-316-622-2	Sequence 2, Appl
25	43.4	68.9	7074	US-09-316-622-1	Sequence 1, Appl
26	43.4	68.9	7129	US-10-047-542-101	Sequence 101, App
27	43.4	68.9	10100	US-09-316-622-5	Sequence 5, Appl
28	43.4	68.9	10100	US-09-316-622-5	Sequence 5, Appl
29	43.4	68.9	10166	US-09-316-622-8	Sequence 8, Appl
30	43.4	68.9	10166	US-09-316-622-8	Sequence 8, Appl
31	43.4	68.9	10240	US-09-316-622-6	Sequence 6, Appl
32	43.4	68.9	10272	US-09-316-622-7	Sequence 7, Appl
33	43.4	68.9	13737	US-10-074-279-10	Sequence 10, Appl
34	43.4	68.9	14446	US-09-810-861B-4	Sequence 4, Appl
35	41.8	66.3	5349	US-09-870-921-7	Sequence 7, Appl
36	41.8	66.3	5611	US-09-870-921-10	Sequence 10, Appl
37	41.8	66.3	6539	US-09-509-945-5	Sequence 5, Appl
38	41.8	66.3	6548	US-09-509-945-4	Sequence 4, Appl
39	41.8	66.3	17458	US-10-055-001A-25	Sequence 25, Appl
40	41.8	66.3	17476	US-10-055-001A-24	Sequence 24, Appl
41	41.8	66.3	17681	US-10-055-001A-26	Sequence 26, Appl
42	41.8	66.3	17862	US-10-055-001A-23	Sequence 23, Appl
43	41.8	66.3	18691	US-10-055-001A-13	Sequence 13, Appl
44	39	61.9	63	US-09-870-375-33	Sequence 33, Appl
45	39	61.9	80	US-09-870-375-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-963-803-13
; Sequence 13, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yello
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803.
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Directional desoxynucleotide building block
US-09-963-803-13
; Query Match 100.0%; Score 63; DB 9; Length 63;
; Best Local Similarity 100.0%; Pred. No. 3e-16;
; Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATCTGCAGACTAGTGTGATGATCTCATCTCAGCTAGGAGGATGACGATGCC 60
DB 1 CATCTGCAGACTAGTGTGATGATCTCATCTCAGCTAGGAGGATGACGATGCC 60
QY 61 ACT 63
DB 61 ACT 63
; RESULT 2
US-09-963-803-7
; Sequence 7, Application US/09963803

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Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT FILING DATE: 2001-09-26
PRIORITY FILING DATE: 1999-03-29
PRIORITY FILING DATE: 1999-03-29
PRIORITY FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 301
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: promoter MP1154
NAME/KEY: promoter
LOCATION: (1)..(301)
OTHER INFORMATION:
US-09-963-803-7
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Query Match
Best Local Similarity 93.7%; Score 59; DB 9; Length 301;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 13 CTGCAGACTAGTGGATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCACT 63
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110 CTGCAGACTAGTGGATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCACT 71
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RESULT 3
US-09-963-803-6
Sequence 6, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT FILING DATE: 2001-09-26
PRIORITY FILING DATE: 1999-03-29
PRIORITY FILING DATE: 1999-03-29
PRIORITY FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 398
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: promoter MP1147
NAME/KEY: promoter
LOCATION: (1)..(398)
OTHER INFORMATION:
US-09-963-803-6
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Query Match
Best Local Similarity 93.7%; Score 59; DB 9; Length 398;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 5 CTGCAGACTAGTGGATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCACT 63
|||||
110 CTGCAGACTAGTGGATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCACT 168
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RESULT 4
US-09-963-803-25
Sequence 25, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT FILING DATE: 2001-09-26
PRIORITY FILING DATE: 1999-03-29
PRIORITY FILING DATE: 1999-03-29
PRIORITY FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 472
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: promoter MP1169
NAME/KEY: promoter
LOCATION: (1)..(472)
OTHER INFORMATION:
US-09-963-803-25
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Query Match
Best Local Similarity 93.7%; Score 59; DB 9; Length 472;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 5 CTGCAGACTAGTGGATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCACT 63
|||||
110 CTGCAGACTAGTGGATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCACT 168
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```
RESULT 5
US-09-963-803-24
Sequence 24, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT FILING DATE: 2001-09-26
PRIORITY FILING DATE: 1999-03-29
PRIORITY FILING DATE: 1999-03-29
PRIORITY FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 541
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: promoter MP1168
NAME/KEY: promoter
LOCATION: (1)..(541)
OTHER INFORMATION:
US-09-963-803-24
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Query Match
Best Local Similarity 93.7%; Score 59; DB 9; Length 541;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 5 CTGCAGACTAGTGGATTGATGTGATATCTCCACTGACGTAAAGGATGACCATGCCACT 63
|||||
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Db 110 CTGCAGACTGATGATGATGATATCTCCACTGACGTGAAGGATGACGATGCCACT 168

RESULT 6

US-09-963-803-23
; Sequence 23, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:

; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; TITLE OF INVENTION: virus and cassava vein mosaic virus

FILE REFERENCE: 184332042

CURRENT APPLICATION NUMBER: US/09/963,803

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: FR 99/03925

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: PCT IB00/00370

PRIOR FILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 23

LENGTH: 604

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

FEATURE:

NAME/KEY: promoter

LOCATION: (1)..(604)

OTHER INFORMATION:

US-09-963-803-23

Query Match

Best Local Similarity 93.7%; Score 59; DB 9; Length 604;

Best Local Similarity 100.0%; Pred. No. 2.5e-14;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 110 CTGCAGACTGATGATGATGATATCTCCACTGACGTGAAGGATGACGATGCCACT 168

RESULT 7

US-09-963-803-14

; Sequence 14, Application US/09963803

; Publication No. US20030028922A1

; GENERAL INFORMATION:

; APPLICANT: Meristem Therapeutics

; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow

; TITLE OF INVENTION: virus and cassava vein mosaic virus

FILE REFERENCE: 184332042

CURRENT APPLICATION NUMBER: US/09/963,803

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: FR 99/03925

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: PCT IB00/00370

PRIOR FILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 14

LENGTH: 79

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

FEATURE:

NAME/KEY: promoter

LOCATION: (1)..(392)

OTHER INFORMATION:

US-09-963-803-14

Query Match

Best Local Similarity 73.0%; Score 46; DB 9; Length 79;

Best Local Similarity 100.0%; Pred. No. 2.8e-09;

Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 110 CTGCAGACTGATGATGATGATATCTCCACTGACGTGAAGGATGACGATGCCACT 168

Db 34 GATTGATGATATCTCCACTGACGTGAAGGATGACGATGCCACT 79

RESULT 8

US-09-963-803-5
; Sequence 5, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:

; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; TITLE OF INVENTION: virus and cassava vein mosaic virus

FILE REFERENCE: 184332042

CURRENT APPLICATION NUMBER: US/09/963,803

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: FR 99/03925

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: PCT IB00/00370

PRIOR FILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 5

LENGTH: 371

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

FEATURE:

NAME/KEY: promoter

LOCATION: (1)..(371)

OTHER INFORMATION:

US-09-963-803-5

Query Match

Best Local Similarity 73.0%; Score 46; DB 9; Length 371;

Best Local Similarity 100.0%; Pred. No. 4.5e-09;

Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 GATTGATGATATCTCCACTGACGTGAAGGATGACGATGCCACT 138

RESULT 9

US-09-963-803-21/c

; Sequence 21, Application US/09963803

; Publication No. US20030028922A1

; GENERAL INFORMATION:

; APPLICANT: Meristem Therapeutics

; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow

; TITLE OF INVENTION: virus and cassava vein mosaic virus

FILE REFERENCE: 184332042

CURRENT APPLICATION NUMBER: US/09/963,803

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: FR 99/03925

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: PCT IB00/00370

PRIOR FILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 21

LENGTH: 392

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

FEATURE:

NAME/KEY: promoter

LOCATION: (1)..(392)

OTHER INFORMATION:

US-09-963-803-21

Query Match

Best Local Similarity 71.4%; Score 45; DB 9; Length 392;

Best Local Similarity 100.0%; Pred. No. 1.2e-08;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 93 GATTGATGATATCTCCACTGACGTGAAGGATGACGATGCCACT 138

OY 18 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAC 62
|||||
Db 278 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAC 234

RESULT 10
US-09-963-803-19

; Sequence 19, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:

; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19

; LENGTH: 393
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: promoter MPr1162

; NAME/KEY: promoter

; LOCATION: (1)..(393)

; OTHER INFORMATION:

US-09-963-803-19

Query Match 71.4%; Score 45; DB 9; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAC 62
|||||
Db 258 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAC 302

RESULT 11
US-09-963-803-20

; Sequence 20, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:

; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20

; LENGTH: 462
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: promoter MPr1163

; NAME/KEY: promoter

; LOCATION: (1)..(462)

; OTHER INFORMATION:

US-09-963-803-20

Query Match 71.4%; Score 45; DB 9; Length 462;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAC 62
|||||
Db 258 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAC 302

RESULT 12
US-09-963-803-22

; Sequence 22, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:

; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22

; LENGTH: 600
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: promoter MPr1165

; NAME/KEY: promoter

; LOCATION: (1)..(600)

; OTHER INFORMATION:

US-09-963-803-22

Query Match 71.4%; Score 45; DB 9; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAC 62
|||||
Db 396 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAC 440

RESULT 13
US-10-012-070A-47

; Sequence 47, Application US/10012070A
; Publication No. US20030077801A1
; GENERAL INFORMATION:

; APPLICANT: Hawkes, Timothy
; APPLICANT: Warner, Simon
; APPLICANT: Bachoo, Satyinder
; APPLICANT: Pickerill, Andrew

; TITLE OF INVENTION: Herbicide Resistant Plants
; FILE REFERENCE: 50490/UST
; CURRENT APPLICATION NUMBER: US/10/012,070A
; PRIOR FILING DATE: 2001-10-29

; PRIOR APPLICATION NUMBER: PCT/GB00/01573
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 47
; LENGTH: 309
; TYPE: DNA

; ORGANISM: Cauliflower mosaic virus

US-10-012-070A-47

Query Match 68.9%; Score 43.4; DB 9; Length 309;
Best Local Similarity 97.8%; Pred. No. 4.9e-08;

	Matches	44,	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	12	CTACGTGATTGATGATATCTCCACTGACGTAAGGATGACGCA	56							
Db	236	CAAGTGATGTGATGTGATATCTCCACTGACGTAAGGATGACGCA	280							

Search completed: May 24, 2003, 15:36:02
Job time : 50.1129 secs

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RESULT 14
US-09-951-470-3
: Sequence 3, Application US/09951470
: Patent No. US20020102582A1
: GENERAL INFORMATION:
: APPLICANT: Levine, Elaine
: TITLE OF INVENTION: Corn Event MON 810 and Compositions and Methods for Detection The
: FILE REFERENCE: 38-21 (52220)B
: CURRENT APPLICATION NUMBER: US/09/951,470
: PRIORITY FILING DATE: 2001-09-13
: PRIOR APPLICATION NUMBER: 60/232,208
: PRIOR FILING DATE: 2000-09-13
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: Patentin version 3.0
: SEQ ID NO 3
: LENGTH: 566
: TYPE: DNA
: ORGANISM: corn
: FEATURE:
: NAME/KEY: DNA
: LOCATION: (1)..(566)
: OTHER INFORMATION: 5' genome+insert sequence
US-09-951-470-3

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Query Match	68.9%;	Score 43.4;	DB 10;	Length 566;
Best Local Similarity	97.8%;	Pred. NO. 5.9e-08;		
Matches 44;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

OY 12 CTAGTGGATTGATGTGATATCTCCACTGACGTAAGGATGACGCA 56
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 435 CAAGTGATTGATGTGATATCTCCACTGACGTAAGGATGACGCA 479

RESULT 15
 US-09-943-692-33
 Sequence 33, Application US/09943692
 Patent No. US20020152496A1
 GENERAL INFORMATION:
 APPLICANT: FISCHHOFF, DAVID A.
 APPLICANT: FUCHS, ROY L.
 APPLICANT: LAVRIK, PAUL B.
 APPLICANT: MCPHERSON, SYLVIA A.
 APPLICANT: PERLAK, FREDERICK J.
 TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
 FILE REFERENCE: MOBP-195--1
 CURRENT APPLICATION NUMBER: US/09/943,692
 CURRENT FILING DATE: 2001-08-31
 PRIOR APPLICATION NUMBER: 09/027,998
 PRIOR FILING DATE: 1998-02-23
 NUMBER OF SEQ ID NOS: 54
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 33
 LENGTH: 661
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Recombinant Cauliflower Mosaic Viral Promoter (CAMV35S)
 US-09-943-692-33

Query Match	68.9%	Score 43.4;	DB 10;	Length 661;
Best Local Similarity	97.8%;	Pred. NO. 6.1e-08;		
Matches 44;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

OY	12	CTAGTGGA	TGATGTG	ATATCTC	CACTGAC	GTAA	GGGATG	ACGCA	56
	1								
Db	524	CAAGTGGA	TGATGTG <td>ATATCTC <td>CACTGAC <td>GTAA <td>GGGATG <td>ACGCA</td> <td>568</td> </td></td></td></td>	ATATCTC <td>CACTGAC <td>GTAA <td>GGGATG <td>ACGCA</td> <td>568</td> </td></td></td>	CACTGAC <td>GTAA <td>GGGATG <td>ACGCA</td> <td>568</td> </td></td>	GTAA <td>GGGATG <td>ACGCA</td> <td>568</td> </td>	GGGATG <td>ACGCA</td> <td>568</td>	ACGCA	568

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 11:30:46 ; Search time 827.806 Seconds

(without alignments)
1232.553 Million cell updates/sec

Title: US-09-963-803-13

Perfect score: 63

Sequence: 1 catgtctgcactgactgtgat.....aaggatgacatgcact 63

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapect 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estbda:*
2: em_estbun:*
3: em_estln:*
4: em_estnu:*
5: em_estoy:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44.8	71.1	193	BH748289	BH748289 SALK_0450
2	43.8	69.5	405	BH747756	BH747756 SALK_0339
3	43.4	68.9	142	BH749349	BH749349 SALK_0477
4	43.4	68.9	153	BH619283	BH619283 SALK_0407
5	43.4	68.9	153	BH747013	BH747013 SALK_0080
6	43.4	68.9	158	BH748291	BH748291 SALK_0451

7	43.4	68.9	165	17	BH747357	BH747357 SALK_0165
8	43.4	68.9	175	17	BH746616	BH746616 SALK_0452
9	43.4	68.9	190	17	BH752801	BH752801 SALK_0193
10	43.4	68.9	214	17	BH747829	BH747829 SALK_0353
11	43.4	68.9	215	17	BH753813	BH753813 SALK_0296
12	43.4	68.9	219	17	BH747744	BH747744 SALK_0337
13	43.4	68.9	220	17	BH747438	BH747438 SALK_0174
14	43.4	68.9	221	17	BH802415	BH802415 100802680
15	43.4	68.9	230	17	BH746474	BH746474 SALK_0428
16	43.4	68.9	230	17	BH799173	BH799173 100802581
17	43.4	68.9	237	17	BH802463	BH802463 100802650
18	43.4	68.9	244	17	BH746375	BH746375 SALK_0402
19	43.4	68.9	248	17	BH254798	BH254798 SALK_0172
20	43.4	68.9	251	17	BH750171	BH750171 SALK_0371
21	43.4	68.9	254	17	BH748500	BH748500 SALK_0460
22	43.4	68.9	256	17	BH748499	BH748499 SALK_0460
23	43.4	68.9	258	17	BH802470	BH802470 1008026F0
24	43.4	68.9	268	17	BH611919	BH611919 SALK_0318
25	43.4	68.9	269	17	BH211646	BH211646 SALK_0064
26	43.4	68.9	271	17	BH799178	BH799178 1008025C0
27	43.4	68.9	272	17	BH802428	BH802428 1008026C0
28	43.4	68.9	274	17	BH802495	BH802495 1008026H0
29	43.4	68.9	279	17	BH748475	BH748475 SALK_0460
30	43.4	68.9	281	17	BH750170	BH750170 SALK_0371
31	43.4	68.9	284	17	BH802443	BH802443 1008026D0
32	43.4	68.9	284	17	BH213307	BH213307 SALK_0090
33	43.4	68.9	284	17	BH746665	BH746665 SALK_0457
34	43.4	68.9	286	17	BH747007	BH747007 SALK_0078
35	43.4	68.9	293	17	BH610310	BH610310 SALK_0083
36	43.4	68.9	296	17	BH213532	BH213532 SALK_0093
37	43.4	68.9	335	17	BH213230	BH213230 SALK_0089
38	43.4	68.9	344	17	BH747662	BH747662 SALK_0323
39	43.4	68.9	350	17	BH747675	BH747675 SALK_0325
40	43.4	68.9	355	17	BH747371	BH747371 SALK_0166
41	43.4	68.9	360	17	BH747123	BH747123 SALK_0107
42	43.4	68.9	369	17	BH212448	BH212448 SALK_0075
43	43.4	68.9	371	17	BH753086	BH753086 SALK_0197
44	43.4	68.9	371	17	BH805388	BH805388 100806F0
45	43.4	68.9	372	17	BH758690	BH758690 SALK_0299

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
SALK_045097.54.25.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_045097.54.25.x, DNA sequence.
ACCESSION
BH748289
VERSION
BH748289.1 GI:18961643
KEYWORDS
SOURCE
ORGANISM
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustoids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
Alonso,J.M., Leisse,T.J., Batajias,P., Chen,H., Cheuk,R., Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmermann,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
CONTACT
Contact: Joseph R. Ecker
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The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckers@salk.edu

This is single pass sequence recovered from the left border of

```

FEATURES
source
    TDNA.
    Class: TDNA tagged.
    Location/Qualifiers
        1..193
            /organism="Arabidopsis thaliana"
            /strain="Columbia 0"
            /db_xref="taxon:3702"
            /clone="SALK_045097.54.25.x"
            /clone_lib="Arabidopsis thaliana TDNA insertion lines"
            /note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"
            be found at http://signal.salk.edu/tdna\_protocols.html"

BASE COUNT
    61 a 48 c 43 g 41 t

ORIGIN
    Query Match 71.1%; Score 44.8; DB 17; Length 193;
    Best Local Similarity 87.5%; Pred. No. 1.5e-05;
    Matches 49; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 CATGTCGACGACTAGTCGATTCGATTCGATTCGATTCGACGACGATGACGATGACGACGA 56
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 67 CATCTCAAGACGACGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 122

RESULT 2
LOCUS BH747756
DEFINITION Arabidopsis thaliana genomic clone SALK_033959.47.55.x, DNA
sequence.
ACCESSION BH747756
VERSION BH747756
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 405)
Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (Signal)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
    1..405
        /organism="Arabidopsis thaliana"
        /strain="Columbia 0"
        /db_xref="taxon:3702"
        /clone="SALK_033959.47.55.x"
        /clone_lib="Arabidopsis thaliana TDNA insertion lines"
        /note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"
        be found at http://signal.salk.edu/tdna\_protocols.html"

BASE COUNT
    105 a 109 c 105 g 86 t

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QY	10	GACATGGATTGATGTGATATCTCCACTGACGTAAGGATGACGCA	56
Db	288	GGCAAGTGATGTGATGTGATATCTCCACTGACGTAAGGATGACGCA	334
RESULT 3			
LOCUS			
DEFINITION			
ACCSSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
TITLE			
JOURNAL			
COMMENT			
REFERENCE			
AUTHORS			
FEATURES			
source			
ORIGIN			
BASE COUNT			
Query Match			
Best Local Similarity			
Matches			
QY	12	CTAGTGATTGATGTGATATCTCCACTGACGTAAGGATGACGCA	56
Db	27	CAAGTGATTGATGTGATATCTCCACTGACGTAAGGATGACGCA	71
RESULT 4			
LOCUS			
DEFINITION			
ACCSSION			
VERSION			

[illegible]

Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckeresalk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .153
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_008070.43.05.x"
/clone.lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html"

BASE COUNT 47 a 37 c 33 g 36 t

ORIGIN

Query Match Best Local Similarity 68.9%; Score 43.4; DB 17; Length 153;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Dy 12 CTAGTGATTGATGTGATATCTCCACGTACGTAAAGGATGACGA 56
| | | | | | | | | | | | | | | | | | | | | | | | | |
BH748291/c 158 bp DNA linear GSS 27-FEB-2002

LOCUS BH748291.c

DEFINITION SALK_045100.51.10.x Arabidopsis thaliana TDNA insertion lines

Arabidopsis thaliana genomic clone SALK_045100.51.10.x, DNA sequence.

BH748291
BH748291 GI:18961648

GSS.
thalae cross.

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; euclidyads; core eucloty;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 158)
Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrihab,
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,U.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Contact: Joseph R. Ecker
Unpublished (2001)

JOURNAL
COMMENT
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckeresalk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .158
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_045100.51.10.x"
/clone.lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at

JOURNAL
COMMENT

Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu

This is single pass sequence recovered from the left border of TDNA.

FEATURES

source
Location/Qualifiers

Class: TDNA tagged.

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/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT
ORIGIN

52 a 52 c 41 g 45 t

Query Match 68.9%; Score 43.4; DB 17; Length 190;

Best Local Similarity 97.8%; Pred. No. 4.5e-05;

Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CTAGTGATGATGATATCTCCACTGACGTAAAGGATGACGA 56

Db 75 CAAGTGATGATGATATCTCCACTGACGTAAAGGATGACGA 119

RESULT 10
BH747829
LOCUS

BH747829 214 bp DNA linear GSS 27-FEB-2002

SAUK_035354.55.75.x Arabidopsis thaliana TDNA insertion lines

Arabidopsis thaliana genomic clone SAUK_035354.55.75.x, DNA

sequence.
Accession BH747829

Version BH747829.1

Keywords GI:18960944

Source GSS.

Organism Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 214)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab

,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.

, Zimmermann,J., and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: eckersalk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .214
/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SAUK_035354.55.75.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT
ORIGIN

58 a 56 c 52 g 48 t

Query Match 68.9%; Score 43.4; DB 17; Length 214;

Best Local Similarity 97.8%; Pred. No. 4.8e-05;

Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CTAGTGATGATGATATCTCCACTGACGTAAAGGATGACGA 56

Db 98 CAAGTGATGATGATATCTCCACTGACGTAAAGGATGACGA 142

RESULT 11
BH753813
LOCUS

BH753813 215 bp DNA linear GSS 27-FEB-2002

SAUK_029677.55.00.x Arabidopsis thaliana TDNA insertion lines

Arabidopsis thaliana genomic clone SAUK_029677.55.00.x, DNA

sequence.

Accession BH753813

Version BH753813.1

Keywords GI:18974308

Source GSS.

Organism Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 215)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab

,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.

, Zimmermann,J., and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

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The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: eckersalk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .215
/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SAUK_029677.55.00.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

be found at http://signal.salk.edu/tdna_protocols.html"

found at http://signal.salk.edu/tdna_protocols.html"

found at http://signal.salk.edu/tdna_protocols.html"

found at http://signal.salk.edu/tdna_protocols.html"

found at http://signal.salk.edu/tdna_protocols.html"

found at http://signal.salk.edu/tdna_protocols.html"

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found at http://signal.salk.edu/tdna_protocols.html"

found at http://signal.salk.edu/tdna_protocols.html"

found at http://signal.salk.edu/tdna_protocols.html"

Query Match	68.9%	Score 43.4	DB 17	Length 221
Best Local Similarity	97.8%	Pred. NO. 4.8e-05		
Matches 44	Conservative	0	Mismatches 1	Indels 0
Gaps				

RESULT	15
BH746474	
LOCUS	BH746474
DEFINITION	BH746474 230 bp DNA linear GSS 27-FEB-2007
ACCESSION	SAIK_042817.55.00.x Arabidopsis thaliana TDNA insertion lines
VERSION	Arabidopsis thaliana genomic clone SAIK_042817.55.00.x, DNA
KEYWORDS	sequence.
SOURCE	BH746474
ORGANISM	BH746474.1 GI:18959589
	GSS.
	thale cress.
	Arabidopsis thaliana

Euariyola; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 230)

Alonso,J.M., Leisste,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab

REFERENCE

AUTHORS

TITLE	Zimmerman, J. and Ecker, J.R. , A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL	Arabidopsis Genome
COMMENT	Unpublished (2001)
	Contact: Joseph R. Ecker

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The Salk Institute for Biological Studies
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Tel.: 858 453 4100 x1752
Fax: 858 558 6379

Email: eckerc@talk.edu
This is single pass sequence recovered from the left border of
TDNA.

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Class: TDNA tagged.
FEATURES             location/Qualifiers
source               1. .230

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/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SAIK 042817.55.00.x"
/clone.lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna\_protocols.html"

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	BASE COUNT	68 a	57 c	49 g	56 t	
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	Best Local Similarity	97.8%;	Pred. No. 4.9e-05;			
	Matches 44:	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
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Dd	115 CAAAGTGATGTGATGTGATTCCTCCACTGACGTAAGGAGTAGACGA	159				

Search completed: May 24, 2003, 15:33:26
Job time : 829.806 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 10:21:51 ; Search time 334.194 Seconds

(without alignments)
5225.021 Million cell updates/sec

Title: US-09-963-803-9

Perfect score: 60
Sequence: 1 agccatgacactctgtgcga.....gacgacacaaatgaagaagaa 60Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*
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2: gb_hlg.*
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5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
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14: gb_vl.*
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16: em_fun.*
17: em_hum.*
18: em_in.*
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20: em_om.*
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41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	60	AX036743	AX036743 Sequence
2	60	100.0	317	AX036737	AX036737 Sequence
3	60	100.0	348	AX036738	AX036738 Sequence
4	60	100.0	392	AX036755	AX036755 Sequence
5	60	100.0	393	AX036753	AX036753 Sequence
6	60	100.0	462	AX036754	AX036754 Sequence
7	60	100.0	600	AX036756	AX036756 Sequence
8	60	100.0	9285	AX093047	AX093047 Sequence
9	60	100.0	15077	AX093052	AX093052 Sequence
10	55.4	92.3	301	AX036741	AX036741 Sequence
11	55.4	92.3	371	AX036739	AX036739 Sequence
12	55.4	92.3	398	AX036740	AX036740 Sequence
13	55.4	92.3	472	AX036759	AX036759 Sequence
14	55.4	92.3	541	AX036758	AX036758 Sequence
15	55.4	92.3	604	AX036757	AX036757 Sequence
16	40.4	67.3	515	AX036736	AX036736 Sequence
17	40.4	67.3	515	AX088388	AX088388 Sequence
18	40.4	67.3	532	AX020213	AX020213 Sequence
19	40.4	67.3	593	AX088390	AX088390 Sequence
20	40.4	67.3	838	AX014764	AX014764 Sequence
21	40.4	67.3	853	AX088389	AX088389 Sequence
22	40.4	67.3	857	AX088391	AX088391 Sequence
23	40.4	67.3	931	AX088392	AX088392 Sequence
24	40.4	67.3	931	AX088393	AX088393 Sequence
25	40.4	67.3	1036	AX014765	AX014765 Sequence
26	40.4	67.3	8158	CVU20341	CVU20341 Sequence
27	40.4	67.3	8159	CVU58751	CVU58751 Sequence
28	40.4	67.3	8340	AX329231	AX329231 Sequence
29	40.4	67.3	8340	AX338536	AX338536 Sequence
30	40.4	67.3	12241	AX412168	AX412168 Sequence
31	40.4	67.3	12241	AC120006	AC120006 Mus muscu
32	27.6	46.0	167852	AC072061	AC072061 Homo sapi
33	27.6	46.0	176454	AC111873	AC111873 Rattus no
34	27.6	46.0	177876	AC124942	AC124942 Rattus no
35	27.6	46.0	227160	AC095908	AC095908 Rattus no
36	27.6	45.3	177648	AC011323	AC011323 Homo sapi
37	27.2	45.3	188193	AL672033	AL672033 Mus muscu
38	27.2	45.3	198468	AC098477	AC098477 Homo sapi
39	27.2	45.3	237560	AL845481	AL845481 Dario fer
40	27	45.0	11953	AL646019	AL646019 Human DNA
41	27	45.0	179694	AC115910	AC115910 Mus muscu
42	26.4	44.0	83167	AL590423	AL590423 Human DNA
43	26.4	44.0	99025	HSPJ45N11	AL132996 Human DNA
44	26.4	44.0	124000	AC004060	AC004060 Homo sapi
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ALIGNMENTS

RESULT 1
AX036743 LOCUS AX036743 60 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 9 from Patent WO0058485.
ACCESSION AX036743
VERSION AX036743.1 GI:11226252
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.
artificial sequences.
REFERENCE
1 (bases 1 to 60)
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
TITLE
JOURNAL
Patent: WO 0058485-A 9 05-OCT-2000;

MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
location/Qualifiers
1. .60
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Directional desoxynucleotide building block 52"

BASE COUNT 25 a 12 c 13 g 10 t
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Best Local Similarity 100.0%; Pred. No. 3.6e-10;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCCATGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACAAACAATGAAAAGAA 60
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Db 1 AGCCATGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACAAACAATGAAAAGAA 60

RESULT 2
AX036737
LOCUS AX036737 317 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 3 from Patent WO0058485.
ACCESSION AX036737
VERSION AX036737.1 GI:11226246
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 317)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 3 05-OCT-2000;
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
location/Qualifiers
1. .317
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter Mp1116"

BASE COUNT 107 a 61 c 74 g 75 t
ORIGIN

promoter 1. .317
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Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 73 AGCCATGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACAAACAATGAAAAGAA 132

RESULT 3
AX036738
LOCUS AX036738 348 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 4 from Patent WO0058485.
ACCESSION AX036738
VERSION AX036738.1 GI:11226247
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 348)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 4 05-OCT-2000;
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
location/Qualifiers
1. .348

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/organism="synthetic construct"
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/note="promoter Mp1117"

Promoter 1. .348
BASE COUNT 116 a 70 c 78 g 84 t
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Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 107 AGCCATGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACAAACAATGAAAAGAA 166

RESULT 4
AX036755
LOCUS AX036755 392 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 21 from Patent WO0058485.
ACCESSION AX036755
VERSION AX036755.1 GI:11226264
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 392)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 21 05-OCT-2000;
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter Mp1116"

BASE COUNT 127 a 80 c 87 g 98 t
ORIGIN

promoter 1. .392
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Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 75 AGCCATGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACAAACAATGAAAAGAA 134

RESULT 5
AX036753
LOCUS AX036753 393 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 19 from Patent WO0058485.
ACCESSION AX036753
VERSION AX036753.1 GI:11226262
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 393)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 19 05-OCT-2000;
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
location/Qualifiers
1. .393
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/db_xref="taxon:32630"
/note="promoter Mp1116"

FEATURES
source

Promoter 1.393
BASE COUNT 128 a 75 c 93 g 97 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 75 AGCCATGACACTCTGTGCGAATATTGAAGACGTAGACGACGACACCAATGAAAGAA 134

RESULT 6
AX036754 462 bp DNA linear PAT 16-NOV-2000
LOCUS Sequence 20 from Patent WO0058485.
ACCESSION AX036754
VERSION AX036754.1 GI:11226263
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 462)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE ChimERIC expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 20 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR) ; GRUBER VERONIQUE (FR)
FEATURES
source 1.462
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter MPRI163"
BASE COUNT 148 a 87 c 111 g 116 t
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Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 75 AGCCATGACACTCTGTGCGAATATTGAAGACGTAGACGACGACCAATGAAAGAA 134

RESULT 7
AX036756 600 bp DNA linear PAT 16-NOV-2000
LOCUS Sequence 22 from Patent WO0058485.
ACCESSION AX036756
VERSION AX036756.1 GI:11226265
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 600)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE ChimERIC expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 22 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR) ; GRUBER VERONIQUE (FR)
FEATURES
source 1.600
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter MPRI165"
BASE COUNT 188 a 111 c 147 g 154 t
ORIGIN

Query Match 100.0%; Score 60; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AGCCATGACACTCTGTGCGAATATTGAAGACGTAGACGACGACCAATGAAAGAA 60
Db 75 AGCCATGACACTCTGTGCGAATATTGAAGACGTAGACGACGACCAATGAAAGAA 134

RESULT 8
AX093047 9285 bp DNA linear PAT 30-MAR-2001
LOCUS Sequence 52 from Patent WO0118192.
ACCESSION AX093047
VERSION AX093047.1 GI:13509522
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 9285)
AUTHORS Gruber,V. and Comeau,D.
TITLE Synthetic vectors, transgenic plants containing them, and methods for obtaining them
JOURNAL Patent: WO 0118192-A 52 15-MAR-2001;
MERISTEM THERAPEUTICS (FR)
FEATURES
source 1.9285
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PMRT1336"
misc_feature 1
/note="PMRT1336 results from the insertion into PMRT1196 of the promoter MPRI165 isolated from plasmid PMRT1332 as described in PCT patent application PCT/IB00/00370"
BASE COUNT 2440 a 2252 c 2506 g 2087 t
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Best Local Similarity 100.0%; Pred. No. 3.2e-10;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AGCCATGACACTCTGTGCGAATATTGAAGACGTAGACGACGACCAATGAAAGAA 60
Db 5864 AGCCATGACACTCTGTGCGAATATTGAAGACGTAGACGACGACCAATGAAAGAA 5923

RESULT 9
AX093052 15077 bp DNA linear PAT 30-MAR-2001
LOCUS Sequence 57 from Patent WO0118192.
ACCESSION AX093052
VERSION AX093052.1 GI:13509527
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 15077)
AUTHORS Gruber,V. and Comeau,D.
TITLE Synthetic vectors, transgenic plants containing them, and methods for obtaining them
JOURNAL Patent: WO 0118192-A 57 15-MAR-2001;
MERISTEM THERAPEUTICS (FR)
FEATURES
source 1.15077
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PMRT1342"
misc_feature 1
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BASE COUNT 3672 a 3892 c 4225 g 3288 t
ORIGIN

Query Match 100.0%; Score 60; DB 6; Length 15077;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 6903 AGCCATGACACTGTGCGAATATTGAAGACGTAGACATGACACAAATGAAAAAGAA 6962

RESULT 10
AX036741 AX036741 301 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 7 from Patent WO0058485.
ACCESSION AX036741
VERSION AX036741 GI:11226250
KEYWORDS

SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 301)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 7 05-OCT-2000;
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
location/Qualifiers

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/db_xref="taxon:32630"
/note="promoter MPr1154"

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Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 63 CATGCCACTGTGCGAATATTGAAGACGTAGACATGACACAAATGAAAAAGAA 119

RESULT 11
AX036739 AX036739 371 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 5 from Patent WO0058485.
ACCESSION AX036739
VERSION AX036739.1 GI:11226248
KEYWORDS

SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 371)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 5 05-OCT-2000;
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
location/Qualifiers

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/note="promoter MPr1146"

BASE COUNT 122 a 68 c 89 g 92 t
ORIGIN

Query Match 92.3%; Score 55.4; DB 6; Length 371;
Best Local Similarity 98.2%; Pred. No. 1.3e-08;
Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 CATGACACTGTGCGAATATTGAAGACGTAGACATGACACAAATGAAAAAGAA 60
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Db 130 CATGCCACTGTGCGAATATTGAAGACGTAGACATGACACAAATGAAAAAGAA 186

RESULT 12
AX036740 AX036740 398 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 6 from Patent WO0058485.
ACCESSION AX036740
VERSION AX036740.1 GI:11226249
KEYWORDS

SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 398)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 6 05-OCT-2000;
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
location/Qualifiers

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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter MPr1147"

BASE COUNT 128 a 80 c 93 g 97 t
ORIGIN

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Best Local Similarity 98.2%; Pred. No. 1.3e-08;
Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 160 CATGCCACTGTGCGAATATTGAAGACGTAGACATGACACAAATGAAAAAGAA 216

RESULT 13
AX036759 AX036759 472 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 25 from Patent WO0058485.
ACCESSION AX036759
VERSION AX036759.1 GI:11226268
KEYWORDS

SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 472)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 25 05-OCT-2000;
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
location/Qualifiers

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/db_xref="taxon:32630"
/note="promoter MPr1169"

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ORIGIN

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Best Local Similarity 98.2%; Pred. No. 1.3e-08;
Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 CATGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACACAATGAAAGAA 60
 Db 160 CATGCACTCTGTGCGAATATTGAAGACGTAGACACTGACGACACAATGAAAGAA 216

RESULT 14
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LOCUS AX036758 541 bp DNA linear PAT 16-NOV-2000
 DEFINITION Sequence 24 from Patent WO0058485.
 ACCESSION AX036758
 VERSION AX036758.1 GI:11226267

KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.

REFERENCE
 1 (bases 1 to 541)
 AUTHORS Rance,I., Theisen,M. and Gruber,V.
 TITLE ChimERIC expression promoters originating from commelina yellow
 Mottle virus and cassava vein mosaic virus
 JOURNAL Patent: WO 0058485-A 24 05-OCT-2000;
 MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
 ; GRUBER VERONIQUE (FR)

FEATURES
 source Location/Qualifiers
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/organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="promoter MP1168"

Promoter 1..541
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 Best Local Similarity 98.2%; Pred. No. 1.3e-08;
 Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 CATGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACACAATGAAAGAA 60
 Db 160 CATGCACTCTGTGCGAATATTGAAGACGTAGACACTGACGACACAATGAAAGAA 216

RESULT 15
 AX036757

LOCUS AX036757 604 bp DNA linear PAT 16-NOV-2000
 DEFINITION Sequence 23 from Patent WO0058485.
 ACCESSION AX036757
 VERSION AX036757.1 GI:11226266

KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.

REFERENCE
 1 (bases 1 to 604)
 AUTHORS Rance,I., Theisen,M. and Gruber,V.
 TITLE ChimERIC expression promoters originating from commelina yellow
 Mottle virus and cassava vein mosaic virus
 JOURNAL Patent: WO 0058485-A 23 05-OCT-2000;
 MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
 ; GRUBER VERONIQUE (FR)

FEATURES
 source Location/Qualifiers
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/organism="synthetic construct"
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Promoter 1..604
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 Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 160 CATGCACTCTGTGCGAATATTGAAGACGTAGACACTGACGACACAATGAAAGAA 216

Db 160 CATGCACTCTGTGCGAATATTGAAGACGTAGACACTGACGACACAATGAAAGAA 216

Search completed: May 24, 2003, 14:52:19
 Job time : 340.194 secs

GenCore version 5.1.4.p5 4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 07:18:51 ; Search time 103.548 Seconds

(Without alignments)
1304.896 Million cell updates/sec

Title: US-09-963-803-9

Perfect score: 60

Sequence: 1 agccatgacactctgtgcga.....gacacacacatgaagaaga 60

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues 4370478

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: N.GeneSeq_101002.*
2: /SID2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
3: /SID2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
4: /SID2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
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6: /SID2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
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9: /SID2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
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11: /SID2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
12: /SID2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
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14: /SID2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
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21: /SID2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
22: /SID2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
25: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	60	21	AAA96843
2	60	100.0	317	21	AAA96837
3	60	100.0	348	21	AAA96838
4	60	100.0	392	21	AAA96855
5	60	100.0	393	21	AAA96853
6	60	100.0	462	21	AAA96854
7	60	100.0	600	21	AAA96856
8	55.4	92.3	301	21	AAA96841
9	55.4	92.3	371	21	AAA96839

10	55.4	92.3	398	21	AAA96840	Nucleotide sequenc
11	55.4	92.3	472	21	AAA96859	Nucleotide sequenc
12	55.4	92.3	541	21	AAA96858	Nucleotide sequenc
13	55.4	92.3	604	21	AAA96857	Nucleotide sequenc
14	40.4	67.3	392	19	AAV14019	CSVMV promoter CVP
15	40.4	67.3	408	19	AAV14031	CSVMV promoter pde
16	40.4	67.3	411	19	AAV14021	CSVMV promoter pde
17	40.4	67.3	418	19	AAV14032	CSVMV promoter pde
18	40.4	67.3	441	19	AAV14033	CSVMV promoter pde
19	40.4	67.3	458	19	AAV14028	CSVMV promoter pde
20	40.4	67.3	468	19	AAV14029	CSVMV promoter pde
21	40.4	67.3	476	19	AAV14053	CSVMV promoter pde
22	40.4	67.3	491	19	AAV14030	CSVMV promoter pde
23	40.4	67.3	515	21	AAE5506	Promoter from inte
24	40.4	67.3	515	22	AAE5505	Nucleotide sequenc
25	40.4	67.3	524	19	AAV14020	CSVMV promoter CVP
26	40.4	67.3	526	19	AAV14018	CSVMV promoter PA.
27	40.4	67.3	532	22	AAV11575	Cassava Vein Mosai
28	40.4	67.3	593	22	AAE5507	Nucleotide sequenc
29	40.4	67.3	853	22	AAE5506	Nucleotide sequenc
30	40.4	67.3	857	22	AAE5508	Nucleotide sequenc
31	40.4	67.3	931	22	AAE5509	Nucleotide sequenc
32	40.4	67.3	931	22	AAE5510	Nucleotide sequenc
33	40.4	67.3	931	22	AAE5510	Nucleotide sequenc
34	40.4	67.3	1839	24	ABL57988	4-Hydroxyphenylpyr
35	40.4	67.3	4677	24	ABL57989	4-Hydroxyphenylpyr
36	40.4	67.3	8187	24	ABL58082	Binary vector PAGI
37	40.4	67.3	8340	24	ABA04755	Binary vector PAGI
38	40.4	67.3	8340	24	ABD24139	PAGI002 binary ve
39	40.4	67.3	12241	24	ABQ73049	Tomato anthocyanin
40	40.4	67.3	12241	24	AA036732	Binary vector DNA
41	37.2	62.0	305	19	AAV14022	CSVMV promoter PC.
42	37.2	62.0	420	19	AAV14026	CSVMV promoter pde
43	25.2	42.0	2022	21	AAE46193	Arabidopsis thalia
44	25.2	42.0	2525	21	AAE45306	Arabidopsis thalia
45	25.2	42.0	2547	21	AAE40898	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAA96843
ID AAA96843: standard; DNA; 60 BP.
AC AAA96843:
XX 19-FEB-2001 (first entry)
DT
DE
XX Directional desoxynucleotide building block 52.
KW Promoter: intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
transgenic plant; ss.
XX
XX Synthetic.
XX WO200058485-A1.
XX 05-OCT-2000.
XX 29-MAR-2000; 2000WO-IB00370.
XX 29-MAR-1999; 99FR-0003925.
XX (MERI-) MERISTEM THERAPEUTICS.
XX Rance I, Gruber V, Theisen M;
XX WPI: 2000-647238/62.
XX Chimeric expression promoter for transgenic plant production, comprises

PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX
PS Disclosure; Page 23; 91pp; English.
XX
CC The present sequence represents a directional desoxyribonucleotide building
CC block, which was used to construct chimeric promoters of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 60 BP; 25 A; 12 C; 13 G; 10 T; 0 other;
Query Match 100.0%; Score 60; DB 21; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.2e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCATGACACTCTGTGCGAATATTGAAGACGTAAAGCAGACACAAACATGAAAAAGAA 60
DB 1 AGCCATGACACTCTGTGCGAATATTGAAGACGTAAAGCAGACACAAACATGAAAAAGAA 60
RESULT 2
AAA96837
ID AAA96837 standard; DNA: 317 BP.
XX
XX AAA96837;
AC
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter Mpr1116.
XX
XX Promoter; intergenic region; Commelina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX
XX Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
XX WO200058485-A1.
PN
PD 05-OCT-2000.
XX
XX 29-MAR-2000; 2000MO-IB00370.
PF
XX
XX 29-MAR-1999; 99FR-0003925.
PR
XX
XX (MERI-) MERISTEM THERAPEUTICS.
PA
XX
XX Rance I, Gruber V, Theisen M;
PI
XX
XX WPI; 2000-647238/62.
DR
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX
PS Claim 5; Page 81; 91pp; English.
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
CC
SQ Sequence 60 BP; 25 A; 12 C; 13 G; 10 T; 0 other;

CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 317 BP; 107 A; 61 C; 74 G; 75 T; 0 other;
Query Match 100.0%; Score 60; DB 21; Length 317;
Best Local Similarity 100.0%; Pred. No. 4.6e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCATGACACTCTGTGCGAATATTGAAGACGTAAAGCAGACACAAACATGAAAAAGAA 60
DB 73 AGCCATGACACTCTGTGCGAATATTGAAGACGTAAAGCAGACACAAACATGAAAAAGAA 132
RESULT 3
AAA96838
ID AAA96838 standard; DNA: 348 BP.
XX
XX AAA96838;
AC
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter Mpr1117.
XX
XX Promoter; intergenic region; Commelina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX
XX Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
XX WO200058485-A1.
PN
PD 05-OCT-2000.
XX
XX 29-MAR-2000; 2000MO-IB00370.
PF
XX
XX 29-MAR-1999; 99FR-0003925.
PR
XX
XX (MERI-) MERISTEM THERAPEUTICS.
PA
XX
XX Rance I, Gruber V, Theisen M;
PI
XX
XX WPI; 2000-647238/62.
DR
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX
XX Claim 5; Page 81; 91pp; English.
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
CC
SQ Sequence 348 BP; 116 A; 70 C; 78 G; 84 T; 0 other;
Query Match 100.0%; Score 60; DB 21; Length 348;

Best Local Similarity 100.0%; Pred. No. 4.7e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCATGACACTCTGTGGGAATATTGAAGACGTAGACACTGACGCAACAATGAAAAAGA 60
DB 107 AGCCATGACACTCTGTGGGAATATTGAAGACGTAGACACTGACGCAACAATGAAAAAGA 166

RESULT 4
AAA96855
ID AAA96855 standard; DNA; 392 BP.

AC AAA96855;

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MPr1164.

XX Promoter; intergenic region; Commelina yellow mottle virus;

KW chimeric expression promoter; plant vascular expression promoter;

KM plant green tissue expression promoter; Cassava vein mosaic virus;

XX transgenic plant; chimera; ss.

OS Chimeric - Commelina yellow mottle virus.

XX Chimeric - Cassava vein mosaic virus.

PN WO200058485-A1.

PD 05-OCT-2000.

PF 29-MAR-2000; 2000WO-IB00370.

PR 29-MAR-1999; 99FR-0003925.

XX (MERI-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Theisen M;

XX WPI; 2000-647238/62.

DR Claim 5; Page 86; 91pp; English.

XX The present sequence represents a chimeric promoter of the invention.

CC The specification describes chimeric expression promoters. These

CC chimeric promoters comprise a nucleic acid sequence which is derived

CC from a first plant promoter, in which a plant vascular expression

CC promoter region is replaced with a nucleic acid sequence derived from

CC a second plant promoter comprising a plant green tissue expression

CC promoter region. Preferably, the first plant promoter originates from

CC Commelina yellow mottle virus, and the second plant promoter originates

CC from the Cassava vein mosaic virus. Especially, the promoters are

CC derived from intergenic regions. The chimeric promoters are useful

CC for producing transgenic plants.

SQ Sequence 392 BP; 127 A; 80 C; 87 G; 98 T; 0 other;

Query Match 100.0%; Score 60; DB 21; Length 392;

Best Local Similarity 100.0%; Pred. No. 4.8e-12;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCATGACACTCTGTGGGAATATTGAAGACGTAGACACTGACGCAACAATGAAAAAGA 60

DB 75 AGCCATGACACTCTGTGGGAATATTGAAGACGTAGACACTGACGCAACAATGAAAAAGA 134

RESULT 5

AAA96853
ID AAA96853 standard; DNA; 393 BP.

XX AAA96853;

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MPr1162.

XX Promoter; intergenic region; Commelina yellow mottle virus;

KW chimeric expression promoter; plant vascular expression promoter;

KM plant green tissue expression promoter; Cassava vein mosaic virus;

XX transgenic plant; chimera; ss.

OS Chimeric - Commelina yellow mottle virus.

XX Chimeric - Cassava vein mosaic virus.

PN WO200058485-A1.

PD 05-OCT-2000.

PF 29-MAR-2000; 2000WO-IB00370.

PR 29-MAR-1999; 99FR-0003925.

XX (MERI-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Theisen M;

XX WPI; 2000-647238/62.

DR Claim 5; Page 85; 91pp; English.

XX The present sequence represents a chimeric promoter of the invention.

CC The specification describes chimeric expression promoters. These

CC chimeric promoters comprise a nucleic acid sequence which is derived

CC from a first plant promoter, in which a plant vascular expression

CC promoter region is replaced with a nucleic acid sequence derived from

CC a second plant promoter comprising a plant green tissue expression

CC promoter region. Preferably, the first plant promoter originates from

CC Commelina yellow mottle virus, and the second plant promoter originates

CC from the Cassava vein mosaic virus. Especially, the promoters are

CC derived from intergenic regions. The chimeric promoters are useful

CC for producing transgenic plants.

SQ Sequence 393 BP; 128 A; 75 C; 93 G; 97 T; 0 other;

Query Match 100.0%; Score 60; DB 21; Length 393;

Best Local Similarity 100.0%; Pred. No. 4.8e-12;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCATGACACTCTGTGGGAATATTGAAGACGTAGACACTGACGCAACAATGAAAAAGA 60

DB 75 AGCCATGACACTCTGTGGGAATATTGAAGACGTAGACACTGACGCAACAATGAAAAAGA 134

RESULT 6

AAA96854
ID AAA96854 standard; DNA; 462 BP.

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MPr1163.

XX Promoter; intergenic region; Commelina yellow mottle virus;

KW chimeric expression promoter; plant vascular expression promoter;

KM plant green tissue expression promoter; Cassava vein mosaic virus;

XX transgenic plant; chimera; ss.

XX OS Chimeric - Commelina yellow mottle virus.
XX OS Chimeric - Cassava vein mosaic virus.
XX PN WO200058485-A1.
XX PD 05-OCT-2000.
XX PF 29-MAR-2000; 2000MO-IB00370.
XX PR 29-MAR-1999; 99FR-0003925.
XX
XX (MERI-) MERISTEM THERAPEUTICS.
XX PI Rance I, Gruber V, Thelsen M;
XX DR WPI; 2000-647238/62.
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX Claim 5: Page 86; 91pp; English.
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
XX Sequence 462 BP; 148 A; 87 C; 111 G; 116 T; 0 other;
SO
Query Match 100.0%; Score 60; DB 21; Length 462;
Best Local Similarity 100.0%; Pred. No. 5e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCATGACACTCTGTGCGAATATTGAAGACGTAGACAGACAAATGAAAAA 60
DB 75 AGCCATGACACTCTGTGCGAATATTGAAGACGTAGACAGACAAATGAAAAA 134
RESULT 7
AAA96856
ID AAA96856 standard; DNA; 600 BP.
XX
XX AAA96856;
XX
XX 19-FEB-2001 (first entry)
XX
XX Nucleotide sequence of chimeric expression promoter MP11165.
XX
XX Promoter; intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX
XX Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
XX WO200058485-A1.
XX
XX 05-OCT-2000.
XX
XX 29-MAR-2000; 2000MO-IB00370.
XX
XX 29-MAR-1999; 99FR-0003925.
PR

XX PA (MERI-) MERISTEM THERAPEUTICS.
XX PI Rance I, Gruber V, Thelsen M;
XX DR WPI; 2000-647238/62.
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX Claim 5; Page 86-87; 91pp; English.
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
XX Sequence 600 BP; 188 A; 111 C; 147 G; 154 T; 0 other;
SO
Query Match 100.0%; Score 60; DB 21; Length 600;
Best Local Similarity 100.0%; Pred. No. 5.3e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCATGACACTCTGTGCGAATATTGAAGACGTAGACAGACAAATGAAAAA 60
DB 75 AGCCATGACACTCTGTGCGAATATTGAAGACGTAGACAGACAAATGAAAAA 134
RESULT 8
AAA96841
ID AAA96841 standard; DNA; 301 BP.
XX
XX AAA96841;
XX
XX 19-FEB-2001 (first entry)
XX
XX Nucleotide sequence of chimeric expression promoter MP11154.
XX
XX Promoter; intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX
XX Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
XX WO200058485-A1.
XX
XX 05-OCT-2000.
XX
XX 29-MAR-2000; 2000MO-IB00370.
XX
XX 29-MAR-1999; 99FR-0003925.
XX
XX (MERI-) MERISTEM THERAPEUTICS.
XX PI Rance I, Gruber V, Thelsen M;
XX DR WPI; 2000-647238/62.
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT

XX PS Claim 5; Page 82; 91pp; English.
XX CC The present sequence represents a chimeric promoter of the invention.
CC CC The specification describes chimeric expression promoters. These
CC CC chimeric promoters comprise a nucleic acid sequence which is derived
CC CC from a first plant promoter, in which a plant vascular expression
CC CC promoter region is replaced with a nucleic acid sequence derived from
CC CC a second plant promoter comprising a plant green tissue expression
CC CC promoter region. Preferably, the first plant promoter originates from
CC CC Commelina yellow mottle virus, and the second plant promoter originates
CC CC from the Cassava vein mosaic virus. Especially, the promoters are
CC CC derived from intergenic regions. The chimeric promoters are useful
CC CC for producing transgenic plants.
SQ Sequence 301 BP; 98 A; 54 C; 74 G; 75 T; 0 other;
Query Match 92.3%; Score 55.4; DB 21; Length 301;
Best Local Similarity 98.2%; Pred. No. 2e-10;
Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DY 4 CATGACACTCTGTGCGAATATTGAAGCAGTACGACGACGACCAATGAAAAGAA 60
DB 63 CATGCCACTCTGTGCGAATATTGAAGCAGTACGACGACGACCAATGAAAAGAA 119
RESULT 9
AAA96839
ID AAA96839 standard; DNA; 371 BP.
XX AAA96839;
AC
XX 19-FEB-2001 (first entry)
DT
XX Nucleotide sequence of chimeric expression promoter MP1146.
DE
XX Promoter; intergenic region; Commelina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
PN MO200058485-A1.
PN
XX 05-OCT-2000.
PD
XX 29-MAR-2000; 2000MO-IB00370.
PF
XX 29-MAR-1999; 99FR-0003925.
PR
XX (MERIT-) MERISTEM THERAPEUTICS.
PA
XX Rance I, Gruber V, Theisen M;
PI
XX WPI; 2000-647238/62.
DR
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX Claim 5; Page 81; 91pp; English.
PS
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus, and the second plant promoter originates

CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
SQ Sequence 371 BP; 122 A; 68 C; 89 G; 92 T; 0 other;
Query Match 92.3%; Score 55.4; DB 21; Length 371;
Best Local Similarity 98.2%; Pred. No. 2.1e-10;
Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DY 4 CATGACACTCTGTGCGAATATTGAAGCAGTACGACGACGACCAATGAAAAGAA 60
DB 130 CATGCCACTCTGTGCGAATATTGAAGCAGTACGACGACGACCAATGAAAAGAA 186
RESULT 10
AAA96840
ID AAA96840 standard; DNA; 398 BP.
XX AAA96840;
AC
XX 19-FEB-2001 (first entry)
DT
XX Nucleotide sequence of chimeric expression promoter MP1147.
DE
XX Promoter; intergenic region; Commelina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
PN MO200058485-A1.
PN
XX 05-OCT-2000.
PD
XX 29-MAR-2000; 2000MO-IB00370.
PF
XX 29-MAR-1999; 99FR-0003925.
PR
XX (MERIT-) MERISTEM THERAPEUTICS.
PA
XX Rance I, Gruber V, Theisen M;
PI
XX WPI; 2000-647238/62.
DR
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX Claim 5; Page 82; 91pp; English.
PS
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
SQ Sequence 398 BP; 128 A; 80 C; 93 G; 97 T; 0 other;
Query Match 92.3%; Score 55.4; DB 21; Length 398;
Best Local Similarity 98.2%; Pred. No. 2.2e-10;
Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DY 4 CATGACACTCTGTGCGAATATTGAAGCAGTACGACGACGACCAATGAAAAGAA 60

[illegible]

```

XX Nucleotide sequence of chimeric expression promoter MP1168.
XX
XX Promoter: intergenic region; Commelina yellow mottle virus;
XX chimeric expression promoter; plant vascular expression promoter;
XX plant green tissue expression promoter; Cassava vein mosaic virus;
XX transgenic plant; chimera; ss.
XX
XX Chimeric - Commelina yellow mottle virus.
XX Chimeric - Cassava vein mosaic virus.
XX
XX WO200058485-A1.
XX
XX 05-OCT-2000.
XX
XX 29-MAR-2000; 2000WO-1B00370.
XX
XX 29-MAR-1999; 99FR-0003925.
XX
XX (MERT-) MERISTEM THERAPEUTICS.
XX
XX Rance I, Gruber V, Theisen M;
XX
XX WPI; 2000-647238/62.
XX
XX Chimeric expression promoter for transgenic plant production, comprises
XX sequence from promoter comprising vascular expression region replaced
XX with sequence from promoter comprising green tissue expression region
XX
XX
XX Claim 5; Page 87-88; 91pp; English.
XX
XX The present sequence represents a chimeric promoter of the invention.
XX The specification describes chimeric expression promoters. These
XX chimeric promoters comprise a nucleic acid sequence which is derived
XX from a first plant promoter, in which a plant vascular expression
XX promoter region is replaced with a nucleic acid sequence derived from
XX a second plant promoter comprising a plant green tissue expression
XX promoter region. Preferably, the first plant promoter originates from
XX Commelina yellow mottle virus, and the second plant promoter originates
XX from the Cassava vein mosaic virus. Especially, the promoters are
XX derived from intergenic regions. The chimeric promoters are useful
XX for producing transgenic plants.
XX
XX Sequence 541 BP; 169 A; 104 C; 130 G; 138 T; 0 other:
XX
XX Query Match 92.3%; Score 55.4; DB 21; Length 541;
XX Best Local Similarity 98.2%; Pred. No. 2.3e-10;
XX Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 4 CATGCACTCTGTGGCAATATGAAAGCGTAGACACTGACGACAATGAAGAAGAA 60
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 160 CATGCCACTCTGTGGCAATATGAAAGACGTAGACACTGACGACAATGAAGAAGAA 216
XX
XX RESULT 13
XX AAA96857
XX ID AAA96857 standard; DNA; 604 BP.
XX
XX AAA96857;
XX
XX 19-FEB-2001 (first entry)
XX
XX Nucleotide sequence of chimeric expression promoter MP1167.
XX
XX Promoter; intergenic region; Commelina yellow mottle virus;
XX chimeric expression promoter; plant vascular expression promoter;
XX plant green tissue expression promoter; Cassava vein mosaic virus;
XX transgenic plant; chimera; ss.
XX
XX Chimeric - Commelina yellow mottle virus.
XX Chimeric - Cassava vein mosaic virus.
XX

```

PN WO200058485-A1.
 XX 05-OCT-2000.
 XX 29-MAR-2000; 2000WO-IB00370.
 XX 29-MAR-1999; 99FR-0003925.
 XX (MERI-) MERISTEM THERAPEUTICS.
 XX Rance I, Gruber V, Theisen M;
 XX WPI; 2000-647238/62.
 DR
 XX Chimeric expression promoter for transgenic plant production, comprises
 PT sequence from promoter comprising vascular expression region, replaced
 PT with sequence from promoter comprising green tissue expression region
 PT
 XX
 XX Claim 5; Page 87; 91pp; English.
 XX
 CC The present sequence represents a chimeric promoter of the invention.
 CC The specification describes chimeric expression promoters. These
 CC chimeric promoters comprise a nucleic acid sequence which is derived
 CC from a first plant promoter, in which a plant vascular expression
 CC promoter region is replaced with a nucleic acid sequence derived from
 CC a second plant promoter comprising a plant green tissue expression
 CC promoter region. Preferably, the first plant promoter originates from
 CC Commelina yellow mottle virus, and the second plant promoter originates
 CC from the Cassava vein mosaic virus. Especially, the promoters are
 CC derived from intergenic regions. The chimeric promoters are useful
 CC for producing transgenic plants.
 XX
 XX Sequence 604 BP; 186 A; 116 C; 145 G; 157 T; 0 other;
 SQ
 Query Match 92.3%; Score 55.4; DB 21; Length 604;
 Best Local Similarity 98.2%; Pred. No. 2.4e-10;
 Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 4 CATGACACCTGTGGCAATATTGAGACGTAGACGTACGACCAATGAAAAGAA 60
 Db 160 CATGCCACTGTGGCAATATTGAGACGTAGACGTACGACCAATGAAAAGAA 216
 |||||
 RESULT 14
 AAV14019
 ID AAV14019 standard; DNA; 392 BP.
 AC AAV14019;
 XX 18-JUN-1998 (first entry)
 XX
 XX CSVMV promoter CVPL.
 DE
 XX Cassava vein mosaic virus; CSVMV; promoter; cultivated crop;
 KM tissue-specific expression control; transgenic plant; ss.
 XX
 XX Cassava vein mosaic virus.
 OS
 XX WO9748819-A1.
 PN
 XX 24-DEC-1997.
 PD
 XX 20-JUN-1997; 97WO-US10376.
 PF
 XX 20-JUN-1996; 96US-0020129.
 PR
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX Beachy RN, De Kochko A, Fauquet C, Verdaguer B;
 PI WPI; 1998-063157/06.
 XX

PT Cassava vein mosaic virus promoter - used to express heterologous
 PT DNA sequences for producing transgenic plants having altered
 PT phenotype(s)
 XX
 XX Claim 2; Page 74; 115pp; English.
 PS
 CC This sequence represents a cassava vein mosaic virus promoter, and
 CC is a nucleic acid molecule of the invention. The promoter is capable of
 CC initiating transcription of an operably linked heterologous nucleic acid
 CC sequence in a plant cell. The CSVMV promoters are active in both monocot
 CC and dicot plant species, and therefore can be readily applied to a
 CC variety of cultivated crops. Although generally constitutive, the
 CC derivative promoters include promoters that can regulate expression in a
 CC tissue-specific manner, and therefore are useful for controlling
 CC expression of heterologous genes in a tissue-specific manner. The
 CC promoters can be used for producing transgenic plants with an altered
 CC phenotype.
 CC
 XX
 XX Sequence 392 BP; 154 A; 64 C; 83 G; 91 T; 0 other;
 SQ
 Query Match 67.3%; Score 40.4; DB 19; Length 392;
 Best Local Similarity 97.6%; Pred. No. 5.1e-05;
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 19 GAAATATTGAAGACGTAGACGTACGACCAATGAAAAGAA 60
 Db 143 GAATCTTGAAGACGTAGACGTACGACCAATGAAAAGAA 184
 |||||
 RESULT 15
 AAV14031
 ID AAV14031 standard; DNA; 408 BP.
 AC AAV14031;
 XX 18-JUN-1998 (first entry)
 XX
 XX CSVMV promoter pdeltaDE2.
 DE
 XX Cassava vein mosaic virus; CSVMV; promoter; cultivated crop;
 KM tissue-specific expression control; transgenic plant; ss.
 XX
 XX Cassava vein mosaic virus.
 OS
 XX WO9748819-A1.
 PN
 XX 24-DEC-1997.
 PD
 XX 20-JUN-1997; 97WO-US10376.
 PF
 XX 20-JUN-1996; 96US-0020129.
 PR
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX Beachy RN, De Kochko A, Fauquet C, Verdaguer B;
 PI WPI; 1998-063157/06.
 DR
 XX Cassava vein mosaic virus promoter - used to express heterologous
 PT DNA sequences for producing transgenic plants having altered
 PT phenotype(s)
 XX
 XX Claim 2; Page 84-85; 115pp; English.
 PS
 CC This sequence represents a cassava vein mosaic virus promoter, and
 CC is a nucleic acid molecule of the invention. The promoter is capable of
 CC initiating transcription of an operably linked heterologous nucleic acid
 CC sequence in a plant cell. The CSVMV promoters are active in both monocot
 CC and dicot plant species, and therefore can be readily applied to a
 CC variety of cultivated crops. Although generally constitutive, the
 CC derivative promoters include promoters that can regulate expression in a
 CC tissue-specific manner, and therefore are useful for controlling
 CC expression of heterologous genes in a tissue-specific manner. The

CC promoters can be used for producing transgenic plants with an altered
CC phenotype.

XX Sequence 408 BP; 161 A; 61 C; 86 G; 100 T; 0 other;
SQ

Query Match	67.3%	Score 40.4	DB 19	Length 408
Best Local Similarity	97.6%	Pred. No. 5	1e-05	
Matches 41; Conservative	0	Mismatches 1	Indels 0	Gaps 0

Qy 19 GAAATATTGAAGACGCTAACGACCTACGACAAACAATGAAAGAA 60
|||||
Db 222 GAATCTTGAAGACGTAAGACACTGACGACAAACAATGAAAGAA 263

Search completed: May 24, 2003, 14:34:41
Job time : 104.548 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 13:52:01 ; Search time 24.8387 Seconds
(without alignments)
740.804 Million cell updates/sec

Title: US-09-963-803-9

Perfect score: 60

Sequence: 1 agcatgacacctctgtcga.....gacgacacacatgaagaagaa 60

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/prodata/1/lna/5B.COMB.seq:*
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4: /cgn2_6/prodata/1/lna/6B.COMB.seq:*
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6: /cgn2_6/prodata/1/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24.2	40.3	3025	US-08-961-527-168	Sequence 168, App
2	23.8	39.7	3715	US-09-085-1998-44	Sequence 44, Appl
3	23.8	39.7	4796	US-09-085-1998-3	Sequence 3, Appl
4	23.6	39.3	1647	US-09-472-971-5	Sequence 5, Appl
5	23.6	39.3	4524	US-09-472-971-7	Sequence 7, Appl
6	23.2	38.7	461	US-09-404-879A-27	Sequence 27, Appl
7	23.2	38.7	1567	US-09-404-879A-74	Sequence 74, Appl
8	23.2	38.7	2627	US-09-404-879A-391	Sequence 391, App
9	22.4	37.3	189	US-08-358-160-139	Sequence 139, App
10	22.4	37.3	7102	US-09-138-024-20	Sequence 20, Appl
11	22.4	37.3	7102	US-09-404-066-20	Sequence 20, Appl
12	22.2	37.0	3087	US-08-967-101-5	Sequence 5, Appl
13	22.2	37.0	3087	US-08-592-541-5	Sequence 5, Appl
14	22.2	37.0	3087	US-09-124-698-5	Sequence 5, Appl
15	22.2	37.0	3087	US-09-127-480-5	Sequence 5, Appl
16	22.2	37.0	3087	US-08-496-841C-5	Sequence 5, Appl
17	22.2	37.0	3087	US-09-124-523-5	Sequence 5, Appl
18	22.2	37.0	621	US-09-221-0178-375	Sequence 375, App
19	22.2	36.7	2407	US-08-885-522-2	Sequence 2, Appl
20	22.2	36.7	2407	US-09-195-391-2	Sequence 2, Appl
21	21.8	36.3	324	US-09-134-001C-12	Sequence 12, Appl
22	21.8	36.3	2225	US-09-276-531-109	Sequence 109, App
23	21.6	36.0	615	US-08-642-807A-22	Sequence 22, Appl
24	21.6	36.0	3930	US-09-162-373-2	Sequence 2, Appl
25	21.6	36.0	3930	US-09-467-946-2	Sequence 2, Appl
26	21.4	35.7	1454	US-09-149-476-302	Sequence 302, App
27	21.4	35.7	13440	US-08-961-527-128	Sequence 128, App

28	21.2	35.3	3800	US-08-965-762-15	Sequence 15, Appl
29	21	35.0	629	US-08-670-186-1	Sequence 1, Appl
30	21	35.0	2102	US-08-235-836C-65	Sequence 65, Appl
31	21	35.0	2126	US-08-235-836C-75	Sequence 75, Appl
32	21	35.0	2258	US-07-720-589-1	Sequence 1, Appl
33	21	35.0	2258	US-08-785-190-1	Sequence 1, Appl
34	21	35.0	2258	US-08-785-190-1	Sequence 1, Appl
35	20.8	34.7	471	PCT-US92-05539-1	Sequence 395, Appl
36	20.8	34.7	606	US-09-134-001C-395	Sequence 133, App
37	20.8	34.7	951	US-09-328-111-133	Sequence 227, App
38	20.8	34.7	963	US-09-071-035-297	Sequence 1602, App
39	20.8	34.7	1524	US-09-134-001C-1602	Sequence 1, Appl
40	20.8	34.7	1524	US-07-752-429E-1	Sequence 1, Appl
41	20.8	34.7	1524	US-07-752-428C-1	Sequence 3, Appl
42	20.8	34.7	1524	US-07-752-428C-3	Sequence 1, Appl
43	20.8	34.7	2238	US-08-742-011-1	Sequence 1, Appl
44	20.8	34.7	2912	US-09-307-143-3	Sequence 3, Appl
45	20.8	34.7	3171	US-08-868-786-5	Sequence 5, Appl
			8878	US-08-206-176-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-961-527-168
Sequence 168, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 168:
SEQUENCE CHARACTERISTICS:
LENGTH: 3025 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: Linear
US-08-961-527-168

Query Match 40.3%; Score 24.2; DB 4; Length 3025;
Best local Similarity 78.4%; Pred. No. 4.9;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY 21 ATATTGAAGACTAAGCACTGACGACACACATGAAAA 57
DB 2120 ATATTGAAGACACATCACTGACTGACTGCTTGAAGA 2156

```

NUMBER OF SEQUENCES:   44
CORRESPONDENCE ADDRESS:
ADDRESSER: Oppedahhl & Larson
STREET: PO Box 5270
CITY: Ftisco
STATE: CO
COUNTRY: USA
ZIP: 80443-5270
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
OPERATING SYSTEM: MS DOS 5.0
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,199B
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Larson, Marina T.
REGISTRATION NUMBER: 32038
REFERENCE/DOCKET NUMBER: UBC.P-013052
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2050
TELEX: (970) 668-2052
INFORMATION FOR SEQ ID NO: 3 :
SEQUENCE CHARACTERISTICS:
LENGTH: 4796
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOCHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: human
FEATURES:
OTHER INFORMATION: cDNA for Huntington-interacting protein
US-09-085-199B-3

Query Match      39.7%; Score 23.8; DB 4; Length 4796;
Best Local Similarity    66.7%; Pred. No. 7.8;
Matches     34; Conservative    0; Mismatches    17; Indels    0; Gaps    0;

OY       10 ACTCTGTCGAATATTGAAGACGTAAAGCACTGACGACAACATAAAGAACA 60
          | ||||| ||| ||||| ||| ||||| ||| ||||| |||
DB       3539 AGTTTGCAACTGTAAGTGAAGAACAGCTGAGAGAAAACAGAAAAAGCAA 3489

RESULT 4
US-09-472-971-5
Sequence 5, Application US/09472971
Patent No. 6197547
GENERAL INFORMATION:
APPLICANT: SOGO, Kazuyo
APPLICANT: YANAGI, Hideki
APPLICANT: YURA, Takashi
TITLE OF INVENTION: TRIGGER FACTOR EXPRESSION PLASMIDS
FILE REFERENCE: 1422-409P
CURRENT APPLICATION NUMBER: US/09/472,971
CURRENT FILING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: JP10-372965
EARLIER FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 1647
TYPE: DNA
ORGANISM: Escherichia coli
US-09-472-971-5

Query Match      39.3%; Score 23.6; DB 4; Length 1647;
Best Local Similarity    65.6%; Pred. No. 7.1;
Matches     32; Conservative    0; Mismatches    14; Indels    0; Gaps    0;
```


ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iyer P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: Ley-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: synthetic DNA fragment
US-08-358-160-139

Query Match 37.3%; Score 22.4; DB 1; Length 189;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 27; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 15 GTGCGAATATTGAAGACGTAGCAGCAGCAACATGAAAGA 59
DB 89 GTGAATGTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 45

RESULT 10
US-09-138-024-20/c
Sequence 20, Application US/09138024A
Patent No. 6004779
GENERAL INFORMATION:
APPLICANT: Bradley, John D.
APPLICANT: Thompson, Craig M.
APPLICANT: Moore, Jeffrey B.
APPLICANT: Mobbe, C. Richard
APPLICANT: Healy, Judith M.
APPLICANT: Donnelly, Caroline E.
TITLE OF INVENTION: REGULATED GENE EXPRESSION IN YEAST
FILE REFERENCE: 0342/1D4690S1
CURRENT APPLICATION NUMBER: US/09/138,024A
CURRENT FILING DATE: 1998-08-21
EARLIER APPLICATION NUMBER: 60/056,719

EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 7102
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Plasmid pzm195
US-09-138-024-20

Query Match 37.3%; Score 22.4; DB 3; Length 7102;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 10 ACTCTGCGAATATTGAAGACGTAGCAGCAGCAACATGAAAGA 57
DB 476 ATTATATCGCAAAATTATTAAGAAAGCAATGAGAAACATTAAAA 429

RESULT 11
US-09-404-066-20/c
Sequence 20, Application US/09404066
Patent No. 6365409
GENERAL INFORMATION:
APPLICANT: Bradley, John D.
APPLICANT: Thompson, Craig M.
APPLICANT: Moore, Jeffrey B.
APPLICANT: Mobbe, C. Richard
APPLICANT: Healy, Judith M.
APPLICANT: Donnelly, Caroline E.
TITLE OF INVENTION: REGULATED GENE EXPRESSION IN YEAST
FILE REFERENCE: 0342/1D4690S1
CURRENT APPLICATION NUMBER: US/09/404,066
CURRENT FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/138,024
PRIOR FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: 60/056,719
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 7102
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Plasmid pzm195
US-09-404-066-20

Query Match 37.3%; Score 22.4; DB 4; Length 7102;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 10 ACTCTGCGAATATTGAAGACGTAGCAGCAGCAACATGAAAGA 57
DB 476 ATTATATCGCAAAATTATTAAGAAAGCAATGAGAAACATTAAAA 429

RESULT 12
US-08-967-101-5/c
Sequence 5, Application US/08967101
Patent No. 5840540
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston

STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3087 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-967-101-5

Query Match 37.0%; Score 22.2; DB 2; Length 3087;
Best Local Similarity 63.5%; Pred. No. 27;
Matches 33; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 9 CACTCTGCGAATTTGAGACGTAAGCACTGAGACACATGAAAGAA 60
DB 375 CACTATGATTAAATANTGCTTAAGCAGAGCTGACCACACGCTGAGAAGAA 324

RESULT 13

US-08-592-541-5/c
Sequence 5, Application US/08592541
Patent No. 5986054

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3087 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-592-541-5

Query Match 37.0%; Score 22.2; DB 2; Length 3087;
Best Local Similarity 63.5%; Pred. No. 27;
Matches 33; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 9 CACTCTGCGAATTTGAGACGTAAGCACTGAGACACATGAAAGAA 60
DB 375 CACTATGATTAAATANTGCTTAAGCAGAGCTGACCACACGCTGAGAAGAA 324

RESULT 14

US-09-124-698-5/c
Sequence 5, Application US/09124698
Patent No. 6117978

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3087 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-124-698-5

Query Match 37.0%; Score 22.2; DB 3; Length 3087;
Best Local Similarity 63.5%; Pred. No. 27;
Matches 33; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 9 CACTCTGCGAATTTGAGACGTAAGCACTGAGACACATGAAAGAA 60
DB 375 CACTATGATTAAATANTGCTTAAGCAGAGCTGACCACACGCTGAGAAGAA 324

RESULT 15

US-09-127-480-5/c
Sequence 5, Application US/09127480
Patent No. 6194153

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3087 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-127-480-5

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: APPLICANT: ST. GEORGE-HYSLOP, PETER H
: APPLICANT: ROMMENS, JOHANNA M
: APPLICANT: FRASER, PAUL E
: TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
: TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
: NUMBER OF SEQUENCES: 183
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: TESTA, HURWITZ & THIBEAULT
: STREET: High Street Tower - 125 High Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02110
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/127,480
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/592,541
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Pitcher, Edmund R.
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 248-7000
: TELEFAX: (617) 248-7100
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3087 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-09-127-480-5

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Query Match          37.0%; Score 22.2; DB 4; Length 3087;
Best Local Similarity 63.5%; Pred. No. 27;
Matches 33; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
OY 9 CACCTCTGTGGCAATATGAGACGTAGCACTGACGACACATGAAAGAA 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 375 CACTATGATTAATTAATGCTTAAGACAGAGCTGACACACGATGAGAGAA 324

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Search completed: May 24, 2003, 15:37:35
 Job time : 27.8387 secs

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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 13:48:31 ; Search time:46.7742 seconds
(without alignments)
1693.834 Million cell updates/sec

Title: US-09-963-803-9

Perfect score: 60
Sequence: 1 agccatgacactctgtgcga.....gacgacaacatgaagaagaa 60

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_NA:*
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10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEM_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	60	9	US-09-963-803-9
2	60	100.0	317	9	US-09-963-803-3
3	60	100.0	348	9	US-09-963-803-4
4	60	100.0	392	9	US-09-963-803-21
5	60	100.0	393	9	US-09-963-803-19
6	60	100.0	462	9	US-09-963-803-20
7	60	100.0	600	9	US-09-963-803-22
8	55.4	92.3	301	9	US-09-963-803-7
9	55.4	92.3	371	9	US-09-963-803-5
10	55.4	92.3	398	9	US-09-963-803-6
11	55.4	92.3	472	9	US-09-963-803-25
12	55.4	92.3	541	9	US-09-963-803-24
13	55.4	92.3	604	9	US-09-963-803-23
14	40.4	67.3	515	9	US-09-963-803-2
15	40.4	67.3	532	9	US-09-765-555-1
16	40.4	67.3	8340	10	US-09-847-057-4
17	40.4	67.3	8340	10	US-09-874-926-4
18	40.4	67.3	12241	12	US-10-033-190-5
19	24.6	41.0	1488	9	US-09-891-641-25

c	20	24.4	40.7	513509	9	US-09-754-853A-4	Sequence 4, Appl1
	21	24.2	40.3	2259	10	US-09-815-242-9323	Sequence 9323, Ap
	22	24.2	40.3	2259	10	US-09-815-242-9563	Sequence 9563, Ap
	23	23.8	38.7	272	10	US-09-850-178-31	Sequence 31, Appl
c	24	23.8	39.7	518	10	US-09-864-761-13307	Sequence 13307, A
	25	23.6	39.3	367	10	US-09-764-877-65	Sequence 65, Appl
	26	23.6	39.3	373	7	US-08-781-986A-1139	Sequence 3139, Ap
	27	23.6	39.3	400	7	US-08-781-986A-3782	Sequence 3782, Ap
	28	23.6	39.3	2155	10	US-09-960-428-13	Sequence 13, Appl
	29	23.6	39.3	4473	10	US-09-815-242-4513	Sequence 4513, Ap
	30	23.6	39.3	4509	10	US-09-815-242-8064	Sequence 8064, Ap
c	31	23.6	39.3	30246	7	US-08-781-986A-56	Sequence 56, Appl
c	32	23.4	39.0	802	10	US-09-867-550-1365	Sequence 1365, Ap
c	33	23.2	38.7	281	10	US-09-850-178-4	Sequence 4, Appl1
	34	23.2	38.7	285	9	US-10-015-219-1338	Sequence 1338, Ap
	35	23.2	38.7	285	10	US-09-777-564-1338	Sequence 1338, Ap
	36	23.2	38.7	352	10	US-09-867-701-6377	Sequence 6377, Ap
c	37	23.2	38.7	391	10	US-09-867-701-3918	Sequence 3918, Ap
c	38	23.2	38.7	422	10	US-09-867-701-4906	Sequence 4906, Ap
c	39	23.2	38.7	426	10	US-09-867-701-4161	Sequence 4161, Ap
c	40	23.2	38.7	442	10	US-09-867-701-2832	Sequence 2832, Ap
c	41	23.2	38.7	461	9	US-09-907-969-27	Sequence 27, Appl
c	42	23.2	38.7	461	10	US-09-884-441-27	Sequence 27, Appl
c	43	23.2	38.7	486	10	US-09-867-701-1482	Sequence 1482, Ap
c	44	23.2	38.7	524	10	US-09-867-701-2301	Sequence 2301, Ap
	45	23.2	38.7	555	10	US-09-833-790-388	Sequence 388, App

ALIGNMENTS

RESULT 1
US-09-963-803-9
Sequence 9, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yello
TITLE OF INVENTION: Virus and cassava vein mosaic virus
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Directional desoxynucleotide building block
US-09-963-803-9
Query Match
Best Local Similarity 100.0%; Score 60; DB 9; Length 60;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGCCATGACACTCTGTGCGAATATTGACAGCGTAACACTGACGACACATGAAAGAA 60
DB 1 AGCCATGACACTCTGTGCGAATATTGACAGCGTAACACTGACGACACATGAAAGAA 60
RESULT 2
US-09-963-803-3
Sequence 3, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yello

;; TITLE OF INVENTION: virus and cassava vein mosaic virus
;; FILE REFERENCE: 184332042
;; CURRENT APPLICATION NUMBER: US/09/963,803
;; CURRENT FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: FR 99/03925
;; PRIOR FILING DATE: 1999-03-29
;; PRIOR APPLICATION NUMBER: PCT IB00/00370
;; PRIOR FILING DATE: 2000-10-05
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 3
;; LENGTH: 317
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Promoter MP1116
;; NAME/KEY: promoter
;; LOCATION: (1)..(317)
;; OTHER INFORMATION:
US-09-963-803-3

Query Match 100.0%; Score 60; DB 9; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCCATGACACTCTGTGGATATTGAAGACGTAAAGCACTGACGACACCAATGAAAGAA 60
Db 73 AGCCATGACACTCTGTGGATATTGAAGACGTAAAGCACTGACGACACCAATGAAAGAA 132

RESULT 3
US-09-963-803-4
;; Sequence 4, Application US/09963803
;; Publication No. US2003028922A1
;; GENERAL INFORMATION:
;; APPLICANT: Meristem Therapeutics
;; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
;; FILE REFERENCE: 184332042
;; CURRENT APPLICATION NUMBER: US/09/963,803
;; CURRENT FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: FR 99/03925
;; PRIOR FILING DATE: 1999-03-29
;; PRIOR APPLICATION NUMBER: PCT IB00/00370
;; PRIOR FILING DATE: 2000-10-05
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 4
;; LENGTH: 348
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: promoter MP1117
;; NAME/KEY: promoter
;; LOCATION: (1)..(348)
;; OTHER INFORMATION:
US-09-963-803-4

Query Match 100.0%; Score 60; DB 9; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCCATGACACTCTGTGGATATTGAAGACGTAAAGCACTGACGACACCAATGAAAGAA 60
Db 107 AGCCATGACACTCTGTGGATATTGAAGACGTAAAGCACTGACGACACCAATGAAAGAA 166

RESULT 4
US-09-963-803-21
;; Sequence 21, Application US/09963803
;; Publication No. US2003028922A1

;; GENERAL INFORMATION:
;; APPLICANT: Meristem Therapeutics
;; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
;; FILE REFERENCE: 184332042
;; CURRENT APPLICATION NUMBER: US/09/963,803
;; CURRENT FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: FR 99/03925
;; PRIOR FILING DATE: 1999-03-29
;; PRIOR APPLICATION NUMBER: PCT IB00/00370
;; PRIOR FILING DATE: 2000-10-05
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 21
;; LENGTH: 392
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Promoter MP1164
;; NAME/KEY: promoter
;; LOCATION: (1)..(392)
;; OTHER INFORMATION:
US-09-963-803-21

Query Match 100.0%; Score 60; DB 9; Length 392;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCCATGACACTCTGTGGATATTGAAGACGTAAAGCACTGACGACACCAATGAAAGAA 60
Db 75 AGCCATGACACTCTGTGGATATTGAAGACGTAAAGCACTGACGACACCAATGAAAGAA 134

RESULT 5
US-09-963-803-19
;; Sequence 19, Application US/09963803
;; Publication No. US2003028922A1
;; GENERAL INFORMATION:
;; APPLICANT: Meristem Therapeutics
;; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
;; FILE REFERENCE: 184332042
;; CURRENT APPLICATION NUMBER: US/09/963,803
;; CURRENT FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: FR 99/03925
;; PRIOR FILING DATE: 1999-03-29
;; PRIOR APPLICATION NUMBER: PCT IB00/00370
;; PRIOR FILING DATE: 2000-10-05
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 19
;; LENGTH: 393
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Promoter MP1162
;; NAME/KEY: promoter
;; LOCATION: (1)..(393)
;; OTHER INFORMATION:
US-09-963-803-19

Query Match 100.0%; Score 60; DB 9; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCCATGACACTCTGTGGATATTGAAGACGTAAAGCACTGACGACACCAATGAAAGAA 60
Db 75 AGCCATGACACTCTGTGGATATTGAAGACGTAAAGCACTGACGACACCAATGAAAGAA 134

RESULT 6

US-09-963-803-20
; Sequence 20, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; TITLE OF INVENTION: Virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MP1163
; NAME/KEY: promoter
; LOCATION: (1)..(462)
; OTHER INFORMATION:
US-09-963-803-20

Query Match 100.0%; Score 60; DB 9; Length 462;
Best Local Similarity 100.0%; Pred. No. 1,36-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACCCATGACACTCTGTGCGAATATTGAAAGCGTAAGCACTGACGACGACAAATGAAAGAA 60
DB 75 ACCCATGACACTCTGTGCGAATATTGAAAGCGTAAGCACTGACGACGACAAATGAAAGAA 134

RESULT 7

US-09-963-803-22
; Sequence 22, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; TITLE OF INVENTION: Virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MP1165
; NAME/KEY: promoter
; LOCATION: (1)..(600)
; OTHER INFORMATION:
US-09-963-803-22

Query Match 100.0%; Score 60; DB 9; Length 600;
Best Local Similarity 100.0%; Pred. No. 1,4e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACCCATGACACTCTGTGCGAATATTGAAAGCGTAAGCACTGACGACGACAAATGAAAGAA 60
DB 75 ACCCATGACACTCTGTGCGAATATTGAAAGCGTAAGCACTGACGACGACAAATGAAAGAA 134

RESULT 8
US-09-963-803-7
; Sequence 7, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; TITLE OF INVENTION: Virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MP1154
; NAME/KEY: promoter
; LOCATION: (1)..(301)
; OTHER INFORMATION:
US-09-963-803-7

Query Match 92.3%; Score 55.4; DB 9; Length 301;
Best Local Similarity 98.2%; Pred. No. 5.7e-11;
Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 CATGACACTCTGTGCGAATATTGAAAGCGTAAGCACTGACGACGACAAATGAAAGAA 60
DB 63 CATGACACTCTGTGCGAATATTGAAAGCGTAAGCACTGACGACGACAAATGAAAGAA 119

RESULT 9
US-09-963-803-5
; Sequence 5, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; TITLE OF INVENTION: Virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MP1146
; NAME/KEY: promoter
; LOCATION: (1)..(371)
; OTHER INFORMATION:
US-09-963-803-5

Query Match 92.3%; Score 55.4; DB 9; Length 371;
Best Local Similarity 98.2%; Pred. No. 6e-11;
Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CATGACACTCTGTGGCATATTTGTAAGACGTAAGACACTGACGACACATGAAAGA 60
|||||
Db 130 CATGCCACTCTGTGGCAATATTGAAGACGTAAAGACACTGACGACACACATGAAAGA 186

RESULT 10
US-09-963-803-6
; Sequence 6, Application US/09963803
; Publication No. US20030028922A1

Query Match	92.3%	Score 55.4	DB 9	Length 358
Best Local Similarity	98.2%	Pred. No. 6.1e-11		
Matches 56; Conservative	0	Mismatches 1	Indels 0	Gaps 0

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RESULT 11
US-09-963-803-25
Sequence 25, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow r
TITLE OF INVENTION: virus and cassava vein mosaic virus
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963, 803
CURRENT FILING DATE: 2001-09-26
PRIORITY APPLICATION NUMBER: FR 99/03925
PRIORITY FILING DATE: 1999-03-29
PRIORITY APPLICATION NUMBER: PCT IB00/00370
PRIORITY FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 472
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: promoter MP1169
NAME/KEY: promoter
LOCATION: (1)..(472)
OTHER INFORMATION:
US-09-963-803-25

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Best Local Similarity	98.2%	Pred. No. 6,4e-11	
Matches	56;	Conservative	0;
		Mismatches	1;
		Indels	0;
		Gaps	0.
Qy	4	CATGCACTCTGTGCGAATATTGAAGACGTAGCACTGCACAAACATGAAAGCA	60
Db	160	CATGCCACTCTGTGCGAATATTGAAGACGTAGCACTGCACAAACATGAAAGCA	216

RESULT 12
US-09-963-803-24

;
; LOCATION: (1)..(541,
; OTHER INFORMATION:
US-09-963-803-24

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Oy      4  CATGACATCTGTCGGATATTGTAAGACGTAGACACATGACACAAATGAAAGAA 60
       1111111111111111111111111111111111111111111111111111111
Db      160 CATGCACATCTGTCGGATATTGTAAGACGTAGACACATGACACAAATGAAAGAA 216
       1111111111111111111111111111111111111111111111111111111

RESULT 13
US-09-963-803-23
/ Sequence 23, Application US/09963803
/ Publication No. US20030028922A1
/ GENERAL INFORMATION:
/ APPLICANT: Meristem Therapeutics
/ TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
/ TITLE OF INVENTION: virus and cassava vein mosaic virus
/ FILE REFERENCE: 184332042
/ CURRENT APPLICATION NUMBER: US/09/963.803
/ CURRENT FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: FR 99/03925
/ PRIOR FILING DATE: 1999-03-29
/ PRIOR APPLICATION NUMBER: PCT IB00/00370
/ PRIOR FILING DATE: 2000-10-05
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 23
/ LENGTH: 604
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: promoter Mp1167
/ NAME/KEY: promoter
/ LOCATION: (1)..(604)
/ OTHER INFORMATION:

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US-09-963-803-23

Query Match 92.3%; Score 55.4; DB 9; Length 604;
Best Local Similarity 98.2%; Pred. No. 6.9e-11;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CATGACACTCTGCGAATATGAGACGTAGACACTGACGACACATGAAAGAA 60
|||||
DB 160 CATGCACTCTGTGGAATATTGAAGACGTAGACACTGACGACACATGAAAGAA 216

RESULT 14
US-09-963-803-2
Sequence 2, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 515
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter from the intergenic region of Cassava Vein Mosaic Virus.
FEATURE:
NAME/KEY: Promoter
LOCATION: (1)..(515)
OTHER INFORMATION:
US-09-963-803-2

Query Match 67.3%; Score 40.4; DB 9; Length 515;
Best Local Similarity 97.6%; Pred. No. 2.1e-05;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 GAATTTGAAGACGTAGACACTGACGACACATGAAAGAA 60
|||||
DB 216 GAATCTTGAAGACGTAGACACTGACGACACATGAAAGAA 257

RESULT 15
US-09-765-555-1
Sequence 1, Application US/09765555
Publication No. US20030037355A1
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: Methods and compositions to modulate
FILE REFERENCE: 27801-20014.40
CURRENT APPLICATION NUMBER: US/09/765,555
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 09/620,897
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 60/177,468
NUMBER OF SEQ ID NOS: 75
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 532
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter C5MV

US-09-765-555-1

Query Match 67.3%; Score 40.4; DB 9; Length 532;
Best Local Similarity 97.6%; Pred. No. 2.1e-05;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 GAATTTGAAGACGTAGACACTGACGACACATGAAAGAA 60
|||||
DB 231 GAATCTTGAAGACGTAGACACTGACGACACATGAAAGAA 272

Search completed: May 24, 2003, 15:35:59
Job time : 47.7742 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 11:30:46 / Search time 788.387 Seconds
(without alignments)
1232.553 Million cell updates/sec

Title: US-09-963-803-9
Perfect score: 60
Sequence: 1 agcagcagcactctgtcga.....gacgacacaaatgaagaagaa 60

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 segs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estln:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
C 1	29.4	49.0	385	9	AU230643 AU230643
C 2	27.2	45.3	424	17	AZ924724 4906.1d55
C 3	27	45.0	667	17	BH108966 RPT-24-3
C 4	26.4	44.0	431	17	AZ389667 IM0150L03
5	26.4	44.0	575	17	AO633949 RPT-11-4
6	26.2	43.7	192	10	AM605446 PM4-DR006

C 7	26.2	43.7	658	17	AZ63393 IM0108G23
C 8	25.8	43.0	540	10	AM215182 up05e09.Y
C 9	25.8	43.0	598	10	AV702705
C 10	25.8	43.0	1085	17	CNS0550K
C 11	25.6	42.7	456	13	BM278807
C 12	25.6	42.7	842	12	BF681368
C 13	25.6	42.7	930	12	BG343357
C 14	25.4	42.3	284	13	B118726
C 15	25.4	42.3	489	13	B1813129
C 16	25.4	42.3	500	13	B1812716
C 17	25.2	42.0	510	17	AZ493220
C 18	25	41.7	326	10	AM836970
C 19	25	41.7	524	13	B1812356
C 20	25	41.7	543	17	DR3B14T
C 21	25	41.7	595	10	BE086841
C 22	25	41.7	595	17	AO500652
C 23	25	41.7	669	17	AO480401
C 24	25	41.7	1529	12	BF302770
C 25	24.8	41.3	414	17	AZ913122
C 26	24.8	41.3	541	17	AO927911
C 27	24.8	41.3	698	17	AZ842321
C 28	24.8	41.3	721	17	AZ305083
C 29	24.6	41.0	205	10	BE158588
C 30	24.6	41.0	291	10	AM232994
C 31	24.6	41.0	379	9	A1548520
C 32	24.6	41.0	419	9	A1976090
C 33	24.6	41.0	433	13	B1288988
C 34	24.6	41.0	538	10	BE096573
C 35	24.6	41.0	538	17	AO693720
C 36	24.6	41.0	563	13	BM421339
C 37	24.6	41.0	563	17	BH766803
C 38	24.6	41.0	605	17	BH766819
C 39	24.6	41.0	627	9	A1411341
C 40	24.6	41.0	634	14	BO198811
C 41	24.6	41.0	639	12	BF358001
C 42	24.6	41.0	643	17	AZ498380
C 43	24.6	41.0	695	14	BO973481
C 44	24.6	41.0	920	17	CNS04N3F
C 45	24.6	41.0	1021	13	BG913244

ALIGNMENTS

RESULT 1
AU230643/C
LOCUS AU230643 RAFL19 Arabidopsis thaliana cDNA clone RAFL19-72-A12 3', mRNA sequence.
DEFINITION AU230643
ACCESSION AU230643
VERSION AU230643.1 GI:19799353
KEYWORDS EST.
SOURCE Thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 385)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Akiyama, K., Enju, A., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinozaki, K., Hayashizaki, Y., and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msekic@rct.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI

and XhoI was ligated to modified Lambda FIC-1 vector (Carinucci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES
Source location/Qualifiers

1.385
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAF19-72-A12"
/clone_1ib="RAF19"
/tissue_type="mixture of silique and flower"
/lab_host="DH10B"
/note="Site_1: BamHI; Site_2: SalI; Subtraction library"

BASE COUNT 121 a 93 c 57 g 114 t
Query Match 49.0%; Score 29.4; DB 9; Length 385;
Best Local Similarity 70.9%; Pred. No. 39;
Matches 39; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 3 CCATGACACTCTGTGCGAATATTGAGACGTAGACACTGACACACATGAAGA 57
Db 337 CCATGACACTCTGTGCGAATATTGAGACGTAGACACTGACACACATGAAGA 283

RESULT 2
AZ924724/c 424 bp DNA linear GSS 01-Apr-2001
LOCUS 4906.1d55c22.s1 Saccharomyces mikatae IFO 1815 Saccharomyces
DEFINITION mikatae genomic clone 4906.1d55c22.s1, DNA sequence.
ACCESSION A2924724
VERSION A2924724.1 GI:13495623
KEYWORDS GSS.
SOURCE Saccharomyces mikatae.
ORGANISM Saccharomyces mikatae.

REFERENCE
AUTHORS

1 (bases 1 to 424)
Cliffen, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T., Gish, W.R., Waterston, R.H. and Johnston, M.
Surveying Saccharomyces genomes to identify functional elements by comparative DNA sequence analysis
Unpublished (2001)

JOURNAL

COMMENT
Contact: Johnston M
Department of Genetics
Washington University Medical School
Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA
Tel: 314 362 2735
Fax: 314 362 7855
Email: mj@genetics.wustl.edu
Class: random plasmid subclone.
Location/Qualifiers

FEATURES
Source 1.424
/organism="Saccharomyces mikatae"
/strain="IFO 1815"
/db_xref="taxon:114525"
/clone="4906.1d55c22.s1"
/clone_1ib="Saccharomyces mikatae IFO 1815"
/note="Random genomic sequence"

BASE COUNT 89 a 123 c 80 g 132 t
ORIGIN

Query Match 45.3%; Score 27.2; DB 17; Length 424;
Best Local Similarity 72.9%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 10 ACTCTGCGCAATATTGAAGACGTAGACACTGACACACATGAAGA 57
Db 342 ACTGAGTGAAGAAAGTCAAAATTTAAGCATTAGACACAAATGAAGA 295

RESULT 3

BH108966/c 667 bp DNA linear GSS 19-JUL-2001
LOCUS RPCI-24-367F11.TJ RPCI-24 Mus musculus genomic clone RPCI-24-367F11
DEFINITION , DNA sequence.
ACCESSION BH108966
VERSION BH108966.1 GI:14941565
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akiret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregorgis, E., Russell, D., de Jong, P., and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)

TITLE
JOURNAL
COMMENT
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhaoe@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 367 row: F column: 11
Seq primer: SP6
Class: BAC ends.

FEATURES
Source location/Qualifiers

1.667
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-367F11"
/clone_1ib="RPCI-24"
/sex="Male"
/cell_type="Spleen/Brain"

/note="Vector: pTRAPAC1; Site_1: BamHI; Site_2: BamHI; RPCI-24 mouse BAC library produced by Pieter de Jong. The library was cloned in the pTRAPAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."
BASE COUNT 247 a 93 c 141 g 186 t
ORIGIN

Query Match 45.0%; Score 27; DB 17; Length 667;
Best Local Similarity 66.1%; Pred. No. 2.3e+02;
Matches 39; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

OY 1 AGCATGACACTCTGTGCGAATATTGAGACGTAGACACTGACACAAATGAAGA 59
Db 295 ACCATGACACTCTGTGCGAATATTGAGACGTAGACACTCTTTCAGACAAATTTTAAAGA 237

RESULT 4
AZ389667/c 431 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0150L03R Mouse 10kb plasmid library Mus musculus genomic
DEFINITION clone UUGC1M0150L03 R, DNA sequence.
ACCESSION AZ389667
VERSION AZ389667.1 GI:10503363
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

TITLE
'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: 1, column: 03
Seq primer: CACACAGAAACACCTATGACC
Class: plasmid ends
High quality sequence stop: 431.

FEATURES
SOURCE
1. 431
Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UDGCM0150L03"
/clone.lib="Mouse 10kb plasmid UDGCM library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (g114732114[gb]AF129072.1), a copy-number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN
95 a 81 c 96 g 159 t

Query Match 44.0%; Score 26.4; DB 17; Length 431;
Best Local Similarity 65.0%; Pred. No. 3.3e+02;
Matches 39; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

OY 1 AGCCATGACACTCTGTCGAAATATTGAAGAGCTAGACGACGACCAACATGAAAGAA 60
Db 67 AACAGTAAACTCAGAGCAAAATGTAATGAATGAATGAAGAAACATGCAAGAA 8

RESULT 5
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

A0633949 575 bp DNA linear GSS 17-JUN-1999
RPCI-11-47811.TV RPCI-11 Homo sapiens genomic clone RPCI-11-47811,
DNA sequence.
A0633949
A0633949.1 GI:5096584
GSS.
human.
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 575)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
J.C.

TITLE
Use of BAC End sequences from Library RPCI-11 for Sequence-Ready
Map Building
Unpublished (1997)
Other-GSS: RPCI-11-47811.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hwe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@tigr.org, med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.

FEATURES
SOURCE
1. 575
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="GDB:7683360"
/db_xref="taxon:9606"
/clone="RPCI-11-47811"
/clone.lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site.1: EcoRI; Site.2: EcoRI;
RPCI-11 Human Male BAC Library"

BASE COUNT
ORIGIN
192 a 115 c 102 g 166 t

Query Match 44.0%; Score 26.4; DB 17; Length 575;
Best Local Similarity 69.2%; Pred. No. 3.5e+02;
Matches 36; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 9 CACTGTGCGCAATATTGAGAGCTAGACGACGACGACCAACATGAAAGAA 60
Db 89 CTCCTTGTGTAGATTCGAGAGCTAGACGACGCTTGAACATGATGAA 140

RESULT 6
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AM605446 192 bp mRNA linear EST 23-MAR-2000
PM4-DT0067-010200-002-b05 DT0067 Homo sapiens CDNA, mRNA sequence.
AM605446
AM605446.1 GI:7310187
EST.
human.
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 192)
HCGP http://www.ludwig.org.br/ORSTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Rui Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=PM4dt2=PM4-DT0067-
010200-002-b05dt3=2000-02-01dt4=1)
Seq primer: puc 18 forward
High quality sequence stop: 118.
Location/Qualifiers
1. 192

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="DR0067"
/dec_stage="Adult"
/note="Organ: Denis-drash; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT      50 a      21 c      61 g      56 t      4 others
ORIGIN
Query Match      43.7%; Score 26.2; DB 10; Length 192;
Best Local Similarity 63.8%; Pred. No. 3.4e+02;
Matches 37; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
OY      3 CCATGACACCTGTCGCGCAATATTGAGACGCTAAGCAGTCGACGACAAACAATGAAAGAA 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      90 CTATGAGCTTTGGTGGGAGAAATATGTTATATGTCANNCCACGACGACCACTGTAACGAA 147

```

RESULT	7
AZ363393	
LOCUS	AZ363393
DEFINITION	AZ363393 658 bp DNA linear GSS 02-OCT-2000 IM0108G2C Mouse 10kb plasmid U08C1M library Mus musculus genomic clone U08C1M0108G23 R, DNA sequence.
ACCESSION	AZ363393
VERSION	AZ363393.1 GI:10477093
KEYWORDS	GSS.
SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 658) Dunn, D., Aoyagi, A., Barber, M., Beacons, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niedermauern, A. and Wright, D., Weiser, R.	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Unpublished (2000)	Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5506
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0108 row: G column: 23
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 658.
Location/Qualifiers
1. 658

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC1M0108G23"
/clone_id="Mouse 10kb plasmid UGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  

/note="Vector: pMD42nv: Purified genomic DNA from M.  

musculus C57BL/6J (male) was obtained from the Jackson  

Laboratory Mouse DNA Resource  

(http://www.jax.org/resources/documents/dnares/). The DNA  

was hydrodynamically sheared by repeated passage through a  

0.005 inch orifice at constant velocity. The sheared DNA  

was blunt end-repaired with T4 DNA polymerase and T4  

polynucleotide kinase. Adaptor oligonucleotides were

```

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (911473211419b1AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT	194	a	165	c	105	g	194	t
ORIGIN								
Query Match		43.7%	Score 26.2;	DB 17;				
Best Local Similarity		79.5%	Pred. No. 4.1e+02;					
Matches 31;	Conservative	0;	Mismatches	8;	Indels	0;	Gaps	0;
Oy	22	TATTGAAGCTTAAGCACTGACGACACAAATCAAAAAGA	60					
DB	1	TAGTGAAGCTGAAGGACTGACAAAGAAAAAAGAAAAGA	39					

RESULT 8					
AM215182/c					
LOCUS	AM215182	540 bp	RNA	linear	EST 06-DEC-1999
DEFINITION	up05e09.y1 NCI-CGAP-Hu30 Mus musculus cDNA clone IMAGE:2651176 5'				
	similar to SW:ERP5_HUMAN Q15084 PROBABLE PROTEIN DISULFIDE				
	ISOMERASE P5 PRECURSOR ;, mRNA sequence.				
ACCESSION	AM215182				
VERSION	AM215182.1	GI:6525793			
KEYWORDS	EST.				
SOURCE	house mouse.				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (pages 1 to 540)	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .		
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
	Tumor Gene Index			
	Unpublished (1997)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgaps-remail.nih.gov			
	Tissue Procurement: Gilbert Smith, Ph.D.			

cDNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-60 GAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LUNL at:
www-bio.llnl.gov/bdrp/image/image.html
 MGI:1031628
 Seq primer: -40RP from GABCO
 High quality sequence stop: 241.
 Location/Qualifiers
 1..340
 /organism="Mus musculus"
 /strain="CZECH II"

Query Match	Score	DB	Length
Best Local Similarity	43.08;	25.8;	540;
	64.38;	Pred. No. 5.2e+02;	


```

/organism="Ascaris suum"
/db xref="taxon:6253"
/clone="As_tgz_67F12"
/clone_lib="Ascaris suum adult male testis germinal zone"
from Alan Scott

```

Query Match	42.7%	Score 25.6;	DB 13;	Length 456;
Best Local Similarity	66.1%	Pred. NO. 5.9e+02;		
Matches 37; Conservative	0;	Mismatches 19;	Indels 0;	Gaps 0;

RESULT 12					
BF681368/c					
LOCUS	BF681368	842 bp	mRNA	linear	EST 21-DEC-2000
DEFINITION	602155557F1 NIH_MGC_83 Homo. sapiens cDNA clone IMAGE:4297263 5',				
	mRNA sequence.				

REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Plimates: Carnivora: Homnidae: Homo.
AUTHORS	1 (pages 1 to 842)
TITLE	NIH-MGC http://mgc.ncl.nih.gov/
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D.

cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LUCM151 row: b column: 16
High quality sequence stop: 593.

```

FEATURES
    source
        Location/Qualifiers
            1..842
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:4297263"
                /clone_1lb="NH_MCC_83"
                /lab_host="DH10B (T1 phage-resistant)"
                /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
                site_1: SfiI (ggcgccctcgccg); Site_2: SfiI (ggcgcatatggc
                ): 5' and 3' adaptors were used in cloning as follows: 5
                adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
                sequence: 5'-ATTCTACAGGCCGACGGCGCCGACATC-dT(30)BN-3'
                (where B = A, C, or G and N = A, C, G, or T). Average
                insert size 0.5-1.0 kb). 14/15 colonies

```

Query Match	42.7%;	Score 25.6;	DB 12;	Length 842;
Best Local Similarity	66.1%;	Pred. No. 6.5e+02;		
Matches 37; Conservative	0;	Mismatches 19;	Indels 0;	Gaps 0;

RESULT_13	
BG343357	
LOCUS	BG343357 930 bp mRNA linear EST_22-OCT-2001
DEFINITION	HY5ME80005I11f Hordeum vulgare pre-anthesis spike EST library

LOCUS BG343357 930 bp mRNA linear EST:22-OCT-2001
DEFINITION HY5ME000511lf Hordeum vulgare pre-anthesis spike EST library
HVCNDN0008 (white to yellow anther) Hordeum vulgare cDNA clone
HY5ME000511lf, mRNA sequence.
ACCESSION BG343357
VERSION BG343357.1 GI:13155686
KEYWORDS EST.
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare

REFERENCE	AUTHORS
1 (bases 1 to 930)	Wing, R., Close, T. J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu

TITLE
JOURNAL
COMMENT

Y., Henry D., Palmer, M., Rambo, T., Simmons, J., Choi, D. W., Fenton
, R. D., Close, S. J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resources
for barley genomics: Morex pre-anthesis spike cDNA library
Unpublished (2001)
Contact: Wing RA

Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel.: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu
total hg bases = 465
Seq primer: AATTACCTCCTACTAAAGG
High quality sequence stop: 590.
Location/Qualifiers

Seq primer: AATTACCCCTCACTAAGG
High quality sequence stop: 590.
Location/Qualifiers
1. .930

```

/organism="Hordium vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMBG000511f"
/clone_lib="Hordium vulgare pre-anthesis spike EST library"
/hvcdna0008 ("white to yellow anther")
/tissue_type="pre-anthesis spike"
/lab_host="SOLR"
/notes="Vector: lambdaZAP; Site_1: EcoRI, Site_2: XhoI;
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spike with awns trimmed were collected at white, green and
yellow anther stages (Fenton). Total RNA was prepared from
each pool, equal quantities of all three RNA pools were
combined, poly(A) RNA was purified from the mixture, one
primary unamplified cDNA library was made, and 1 million
pfu were in vivo excised to give phluescript SK(-) cDNA
phageids. These steps were performed in the TJ Close lab
(chol) at the University of California, Riverside.
Phageids were plated and picked at the Clemson University
Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins
and Wang) Plasmid DNA preparations, DNA sequencing and
sequence analysts were performed at CUGI (Wang, Yu, Frisch
Henry, Simmons, Oates, Rambo, Main). The sequence has
been trimmed to remove vector sequence and contains a

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minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinbois A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html>)"

BASE COUNT 240 a 245 c 257 g 180 t 8 others

Query Match 42.7%; Score 25.6; DB 13; Length 930;
Best Local Similarity 64.2%; Pred. No. 6.6e+02;
Matches 34; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 8 ACACCTGTGCAGATATGAGACGTAGCACTGACGACACAAATGAAAGAA 60
B118726
Db 527 ACACGGGTGTGACTTNTNAGACAGAAANNATATTAAGAAAAAGAA 579

RESULT 14
LOCUS B118726 284 bp mRNA linear EST 26-JUN-2001
DEFINITION EST112 Differentially expressed cDNA libraries of BRH-treated/blast fungus-infected rice leaf tissues Oryza sativa cDNA clone BHNH-07, mRNA sequence.

ACCESSION B118726
KEYWORDS B118726.1 GI:14571358
SOURCE EST.
ORGANISM Oryza sativa.

REFERENCE Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 284)
Song, F.M. and Goodman, R.M.
Molecular cloning of differentially expressed cDNAs associated with systemic acquired resistance in rice unpublished (2001)

JOURNAL CONTACT: Song, F.M.; Goodman, R.M.
DEPARTMENT OF PLANT PATHOLOGY
UNIVERSITY OF WISCONSIN-MADISON
RM 689, Russell Laboratories, 1630 Linden Drive, Madison, WI 53706, USA

TELE: 608 262 9162
FAX: 608 262 8643
Email: fmsong@plantpath.wisc.edu; rgoodman@staff.wisc.edu
Benzochladiazole-inducible
Insert Length: 284 Std Error: 0.00
Seq primer: M13 Forward and reverse.

FEATURES
SOURCE Location/Qualifiers

1. 284
/organism="Oryza sativa"
/cultivar="Yuanfengzao (a susceptible variety to rice blast disease)"
/db_xref="taxon:4530"
/clone_lib="BHNH-07"
/clone_lib="Differentially expressed cDNA libraries of BRH-treated/blast fungus-infected rice leaf tissues"
/tissue_type="Seedling leaves"
/dev_stage="Three-week-old rice seedlings pretreated with BRH and/or inoculated with Magnaporthe grisea"
/note="Vector: pGEM-T Easy; Rice seedlings were pretreated by foliar spraying with 0.3 mM benzochladiazole (BRH) and then inoculated with Magnaporthe grisea three days after BRH treatment. Leaf samples were collected twenty-four hour after inoculation and mRNAs were used for construction of the differentially expressed cDNA libraries by suppression subtractive hybridization."

BASE COUNT 80 a 77 c 65 g 62 t

Query Match

42.3%; Score 25.4; DB 13; Length 284;

Best Local Similarity 64.4%; Pred. No. 6.3e+02;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

OY 2 GCCATGACACTGTGTCGCAATATTGAGACGTAGCACTGACGACAAATGAAAGAA 60
B118726
Db 125 GCTGTGTGACTGTGTCGAGTGAAGAGACGACGACGACGACGACGCTTAAAGCA 183

RESULT 15
B1813129/c

LOCUS B1813129 489 bp mRNA linear EST 01-NOV-2001
DEFINITION J002C12 Oryza sativa mature leaf library induced by M.grisea Oryza sativa cDNA clone J002C12, mRNA sequence.

ACCESSION B1813129
KEYWORDS B1813129.1 GI:16579034
SOURCE EST.
ORGANISM Oryza sativa.

Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 489)
Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.
A Gene Expression Screen in Oryza sativa unpublished (2001)

JOURNAL CONTACT: Dong HT
LABORATORY OF FUNCTIONAL GENETICS
BIO-TECHNOLOGY INSTITUTE OF ZHEJIANG UNIVERSITY
KAIHUAN ROAD 268#, HANGZHOU, ZHEJIANG, P.R.CHINA
TEL: 0086-571-86892051
FAX: 0086-571-86961525
Email: ht dong@zjuem.zju.edu.cn
Seq primer: M13 forward primer.

FEATURES
SOURCE Location/Qualifiers

1. 489
/organism="Oryza sativa"
/db_xref="taxon:4530"
/clone_lib="J002C12"
/clone_lib="Oryza sativa mature leaf library induced by M.grisea"
/tissue_type="leaf"
/dev_stage="Mature stage"
/note="Vector: pSport2"

BASE COUNT 134 a 108 c 131 g 116 t

Query Match 42.3%; Score 25.4; DB 13; Length 489;
Best Local Similarity 64.4%; Pred. No. 6.8e+02;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

OY 2 GCCATGACACTGTGTCGCAATATTGAGACGTAGCACTGACGACAAATGAAAGAA 60
B118726
Db 290 GCTGTGTGACTGTGTCGAGTGAAGAGACGACGACGACGACGACGCTTAAAGCA 232

Search completed: May 24, 2003, 15:33:20
Job time : 793.387 secs

